

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.39627 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-20

Perfect score: 1992

Sequence: 1 MHFTQVLISLVLACGPVG.....KEQIIYKIPSMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284.5	14.3	391	1	US-10-517-544-77
2	253	12.7	431	1	US-10-816-768-39
3	237	11.9	366	7	US-11-091-334-9
4	233	11.7	203	1	US-10-816-768-100
5	227.5	11.4	102	1	US-10-816-768-47
6	227.5	11.4	102	1	US-10-816-768-85
7	226.5	11.4	102	1	US-10-816-768-86
8	225.5	11.3	102	1	US-10-816-768-46
9	224.5	11.3	102	1	US-10-816-768-84
10	224	11.2	117	1	US-10-816-768-69
11	224	11.2	139	1	US-10-816-768-68
12	224	11.2	364	1	US-10-131-826A-342
13	224	11.2	364	7	US-11-091-334-2
14	223.5	11.2	102	1	US-10-816-768-88
15	223.5	11.2	129	1	US-10-816-768-89
16	223	11.2	429	1	US-10-967-457-74
17	220.5	11.1	102	1	US-10-816-768-53
18	219.5	11.0	106	1	US-10-816-768-62
19	219.5	11.0	106	1	US-10-816-768-63
20	216.5	10.9	102	1	US-10-816-768-83
21	216.5	10.9	102	1	US-10-816-768-87
22	212.5	10.7	98	1	US-10-816-768-41
23	212	10.6	101	1	US-10-816-768-49
24	211.5	10.6	98	1	US-10-816-768-42
25	211.5	10.6	102	1	US-10-816-768-55

26	210	10.5	101	1	US-10-816-768-59	Sequence 59, Appl
27	207.5	10.4	102	1	US-10-816-768-52	Sequence 52, Appl
28	204.5	10.3	102	1	US-10-816-768-56	Sequence 56, Appl
29	200	10.0	101	1	US-10-816-768-51	Sequence 51, Appl
30	198	9.9	103	1	US-10-816-768-50	Sequence 50, Appl
31	197.5	9.9	102	1	US-10-816-768-45	Sequence 45, Appl
32	196.5	9.9	98	1	US-10-816-768-44	Sequence 44, Appl
33	195.5	9.8	98	1	US-10-816-768-64	Sequence 43, Appl
34	189.5	9.5	98	1	US-10-816-768-40	Sequence 40, Appl
35	188.5	9.5	98	1	US-10-816-768-58	Sequence 38, Appl
36	185	9.3	107	1	US-10-816-768-57	Sequence 58, Appl
37	181.5	9.1	102	1	US-10-816-768-48	Sequence 47, Appl
38	180.5	9.1	118	1	US-10-816-768-9	Sequence 9, Appl
39	176	8.8	35	1	US-10-816-768-54	Sequence 54, Appl
40	166	8.3	103	1	US-10-816-768-54	Sequence 60, Appl
41	147.5	7.4	102	1	US-10-816-768-60	Sequence 65, Appl
42	125.5	6.3	104	1	US-10-816-768-65	Sequence 61, Appl
43	116	5.8	105	1	US-10-816-768-115	Sequence 115, App
44	113	5.7	39	1	US-10-816-768-119	Sequence 119, App
45	111	5.6	39	1	US-10-816-768-119	

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-517-544-77

Query Match	14.3%	Score 284.5;	DB 1;	Length 391;
Best Local Similarity	25.9%	Pred. No. 1.1e-22;		
Matches	97;	Conservative	66;	Mismatches 157; Indels 55; Gaps 14;
QY	41	STCEP--RQHSKLMRLHAIKSQILSKLKAQPNISRDVVKKQLLPKAPLQQLLOYD--	96	
DB	31	STCKTIDMELVKRKRKIEAIRGQILSKLRLASPPSQE-----VPPGPLEAVLALYNST	84	
QY	97	---VLGDDSKGAVZEDDEHATTETIMTATEPDDIVQVDRKPKCFPSFKIQANRTV	153	
DB	85	RDRVAGESAEPEPEADYAKVTRVLMTVETHNIEYDKFKQSTHSIYFFNTSEUREAV	144	
QY	154	-----RAQLWHLR---PAEEATTVFLQISRLMPKDGGRHRRIRSLKIDYNAVTSWQ	203	
DB	145	PEPVLLSRAELRLRLRLKLVKQHVLYQKYS-----NNSRWYLSNELLAPSDSEPL	197	
QY	204	SIDVQKVLTVMLKQETNVRGIEINAY---DAKNDLAV--TSTETGEGDGL-----P	250	
DB	198	SFDTGVVVRQMLSRGSEIEGFRLSAHSCDSRDNTLQVDINGFTTGRGDLATIHGMNRP	257	
QY	251	FM-----EVKISEGPKRIRRSGLDCDCE--NSSESRCRCRYLTVDP-EDFGHWDIIAPKR	302	
DB	258	FLLMATPLERAQHLQSSRRRLDNTNYCFSTKXNCCVQQLYIDFRKDLGKWKWIHEPKG	317	
QY	303	YKANYCSGECDTMYLQKYPHTH---LVNKASPRGTAGPCCTPTKMSPINMLYFNKGKQII	359	

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OM protein - protein search, using sw model

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2359.729 Million cell updates/sec

Title: US-09-628-112-20

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Sequence: 1 MHFTQVLSLSVLIACGPVG.....KEQIIYKIPSMVDRCGCS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:*
- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
 - 4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
 - 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	374	3	US-09-841-730-20
2	1992	100.0	374	4	US-10-662-438-8
3	1992	100.0	374	5	US-10-665-374-8
4	1992	100.0	374	5	US-10-991-343-29
5	1989	99.8	374	4	US-10-074-152-36
6	1367.5	68.6	375	3	US-09-454-540-5
7	1367.5	68.6	375	3	US-09-859-211-14
8	1367.5	68.6	375	3	US-09-841-730-2
9	1367.5	68.6	375	3	US-09-872-856-14
10	1367.5	68.6	375	3	US-09-871-604-5
11	1367.5	68.6	375	4	US-10-074-152-29
12	1367.5	68.6	375	4	US-10-278-803-14
13	1367.5	68.6	375	4	US-10-071-499A-1
14	1367.5	68.6	375	4	US-10-335-483-14
15	1367.5	68.6	375	4	US-10-251-115-8
16	1367.5	68.6	375	4	US-10-253-532-130
17	1367.5	68.6	375	4	US-10-366-345-51
18	1367.5	68.6	375	4	US-10-463-973-14
19	1367.5	68.6	375	4	US-10-456-852-4
20	1367.5	68.6	375	4	US-10-459-127-5
21	1367.5	68.6	375	4	US-10-662-438-2
22	1367.5	68.6	375	5	US-10-689-677C-2
23	1367.5	68.6	375	5	US-10-665-374-2
24	1367.5	68.6	375	5	US-10-997-809-14
25	1367.5	68.6	375	5	US-10-991-343-14
26	1367.5	68.6	375	6	US-11-019-001-1
27	1367.5	68.6	376	3	US-09-813-398-38

28	1367.5	68.6	376	5	US-10-826-324-38	Sequence 38, Appl
29	1363.5	68.4	374	3	US-09-841-730-8	Sequence 8, Appl
30	1363.5	68.4	375	3	US-09-859-211-23	Sequence 23, Appl
31	1363.5	68.4	375	3	US-09-872-856-23	Sequence 23, Appl
32	1363.5	68.4	375	4	US-10-463-973-23	Sequence 23, Appl
33	1363.5	68.4	375	4	US-10-456-852-10	Sequence 10, Appl
34	1363.5	68.4	375	4	US-10-662-438-6	Sequence 6, Appl
35	1363.5	68.4	375	5	US-10-665-374-6	Sequence 6, Appl
36	1362.5	68.4	375	3	US-09-859-894A-5	Sequence 5, Appl
37	1360.5	68.3	375	4	US-10-074-152-34	Sequence 34, Appl
38	1358.5	68.2	375	3	US-09-859-211-27	Sequence 27, Appl
39	1358.5	68.2	375	3	US-09-841-730-18	Sequence 18, Appl
40	1358.5	68.2	375	3	US-09-872-856-27	Sequence 27, Appl
41	1358.5	68.2	375	4	US-10-278-803-19	Sequence 19, Appl
42	1358.5	68.2	375	4	US-10-463-973-27	Sequence 27, Appl
43	1358.5	68.2	375	4	US-10-456-852-14	Sequence 14, Appl
44	1357.5	68.1	375	3	US-09-859-211-19	Sequence 19, Appl
45	1357.5	68.1	375	3	US-09-859-211-29	Sequence 29, Appl

RESULT 1
US-09-841-730-20
; Sequence 20, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS, AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Danio rerio
US-09-841-730-20

Query Match 100.0%; Score 1992; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.1e-178;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MHFTQVLSLSVLIACGPVGVDITAHQOPSTATSEELSCSTCEPRQHSKMLRLHAIKSO	60
Db	1	MHFTQVLSLSVLIACGPVGVDITAHQOPSTATSEELSCSTCEPRQHSKMLRLHAIKSO	60
Qy	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQQLDDQVLDGDDSKGAVEDEDDHATTETIM	120
Db	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQQLDDQVLDGDDSKGAVEDEDDHATTETIM	120
Qy	121	TNATEPDPFIVQDRKPKCCFFSFKPIQANRIVRAQLWVHLRPABEATTVFLOISRLMPV	180
Db	121	TNATEPDPFIVQDRKPKCCFFSFKPIQANRIVRAQLWVHLRPABEATTVFLOISRLMPV	180
Qy	181	KDGGHRRISLIDYNAGVTSKQSDVKQVLTVMWKQPETNRGIGINAYDAKGNDLAVTS	240
Db	181	KDGGHRRISLIDYNAGVTSKQSDVKQVLTVMWKQPETNRGIGINAYDAKGNDLAVTS	240
Qy	241	TETGDLGLPFMEVKISGPKRIRDSGLDCCDENSESSRCRCRYPLTVDPDFGWDWIAP	300
Db	241	TETGDLGLPFMEVKISGPKRIRDSGLDCCDENSESSRCRCRYPLTVDPDFGWDWIAP	300

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.2512 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-20
Perfect score: 1992
Sequence: 1 MHFTQVLSLSVLIACGPVG.....KEQIIYKIPSMVDRCGS 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5 COMB.pap.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pap.*
3: /cgn2_6/prodata/1/iaa/H COMB.pap.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pap.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/prodata/1/iaa/backfilees1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	374	2	US-09-378-238-29
2	1992	100.0	374	2	US-09-626-896-20
3	1992	100.0	374	2	US-09-841-730-20
4	1989	99.8	374	2	US-09-252-149B-36
5	1367.5	68.6	375	1	US-08-525-596B-14
6	1367.5	68.6	375	1	US-08-765-875-5
7	1367.5	68.6	375	2	US-08-795-671-5
8	1367.5	68.6	375	2	US-09-177-860A-14
9	1367.5	68.6	375	2	US-09-252-149B-29
10	1367.5	68.6	375	2	US-09-378-238-14
11	1367.5	68.6	375	2	US-09-451-501-14
12	1367.5	68.6	375	2	US-09-629-938-14
13	1367.5	68.6	375	2	US-09-454-540-5
14	1367.5	68.6	375	2	US-09-686-344-14
15	1367.5	68.6	375	2	US-09-626-896-2
16	1367.5	68.6	375	2	US-09-485-046-4
17	1367.5	68.6	375	2	US-10-278-803-14
18	1367.5	68.6	375	2	US-09-841-730-2
19	1363.5	68.4	374	2	US-09-626-896-8
20	1363.5	68.4	374	2	US-09-841-730-8
21	1363.5	68.4	375	2	US-09-686-344-23
22	1363.5	68.4	375	2	US-09-485-046-10
23	1360.5	68.3	375	2	US-09-252-149B-34
24	1358.5	68.2	375	2	US-09-451-501-19
25	1358.5	68.2	375	2	US-09-686-344-27
26	1358.5	68.2	375	2	US-09-626-896-18
27	1358.5	68.2	375	2	US-09-485-046-14

28	1358.5	68.2	375	2	US-10-278-803-19	Sequence 19, Appl
29	1358.5	68.2	375	2	US-09-841-730-18	Sequence 18, Appl
30	1357.5	68.1	375	2	US-09-252-149B-30	Sequence 30, Appl
31	1357.5	68.1	375	2	US-09-686-344-19	Sequence 19, Appl
32	1357.5	68.1	375	2	US-09-686-344-29	Sequence 29, Appl
33	1357.5	68.1	375	2	US-09-626-896-10	Sequence 10, Appl
34	1357.5	68.1	375	2	US-09-626-896-14	Sequence 14, Appl
35	1357.5	68.1	375	2	US-09-485-046-6	Sequence 6, Appl
36	1357.5	68.1	375	2	US-09-841-730-10	Sequence 10, Appl
37	1357.5	68.1	375	2	US-09-841-730-14	Sequence 14, Appl
38	1355.5	68.0	375	2	US-09-252-149B-35	Sequence 35, Appl
39	1354.5	68.0	375	2	US-09-252-149B-32	Sequence 32, Appl
40	1347.5	67.6	375	2	US-09-451-501-23	Sequence 23, Appl
41	1347.5	67.6	375	2	US-10-278-803-23	Sequence 23, Appl
42	1345.5	67.5	375	2	US-09-686-344-31	Sequence 31, Appl
43	1345.5	67.5	375	2	US-09-626-896-16	Sequence 16, Appl
44	1345.5	67.5	375	2	US-09-841-730-16	Sequence 16, Appl
45	1345.5	67.5	376	1	US-08-525-596B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-378-238-29
; Sequence 29, Application US/09378238
; Patent No. 6465239
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
; FILE OF INVENTION: JHU1120-9
; CURRENT APPLICATION NUMBER: US/09/378, 238
; EARLIER FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 08/795, 071
; EARLIER FILING DATE: 1997-02-05
; EARLIER APPLICATION NUMBER: 08/525, 596
; EARLIER FILING DATE: 1995-10-25
; EARLIER APPLICATION NUMBER: PCT/US94/03019
; EARLIER FILING DATE: 1994-03-18
; EARLIER APPLICATION NUMBER: 08/033, 923
; EARLIER FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Danio rerio
US-09-378-238-29

Query Match	100.0%;	Score	1992;	DB	2;	Length	374;
Best Local Similarity	100.0%;	Pred. No.	1.7e-199;				
Matches	374;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	MHFTQVLSLSVLIACGPVGVDITAHQOPSTATSESELCTCFRQHSKMLRLHAISKQ	60				
Db	1	MHFTQVLSLSVLIACGPVGVDITAHQOPSTATSESELCTCFRQHSKMLRLHAISKQ	60				
Qy	61	ILSKRLKQAPNISRDVVKQLLPKAPPLQQLDQYDVLGDDSKDGAVEDEDEHATTETIM	120				
Db	61	ILSKRLKQAPNISRDVVKQLLPKAPPLQQLDQYDVLGDDSKDGAVEDEDEHATTETIM	120				
Qy	121	TMATEPDPVQDRKPKCCFFSPKIQANRIVRAQLWHLRPAEATTVFLQISRLMPV	180				
Db	121	TMATEPDPVQDRKPKCCFFSPKIQANRIVRAQLWHLRPAEATTVFLQISRLMPV	180				
Qy	181	KDGRHRIRSLKIDVNAVGTWSQIDVKQVLTWVKQPETNRGIEINAYDKGNDLAVTS	240				
Db	181	KDGRHRIRSLKIDVNAVGTWSQIDVKQVLTWVKQPETNRGIEINAYDKGNDLAVTS	240				
Qy	241	TETGEDGLLPFMEVKISEGPKIRIRDSGLDCDENSESSESCCRYPYLTVPDFDQWDIIAP	300				

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302.622 Million cell updates/sec

Title: US-09-628-112-18
Perfect score: 2014
Sequence: 1 MQLAVVYVYLFQMQLVHP.....KEQIIYKIPAMVDRGCS 375

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Maximum Match 100%
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1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pbp:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pbp:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pbp:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pbp:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pbp:*
6: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pbp:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	257	12.8	431	1	US-10-816-768-39
3	239	11.9	429	1	US-10-967-457-74
4	236	11.7	364	1	US-10-131-826A-342
5	236	11.7	364	7	US-11-091-334-2
6	234.5	11.6	366	7	US-11-091-334-9
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	203	1	US-10-816-768-69
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5'end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.5%	Score 312.5;	DB 1;	Length 391;
Best Local Similarity	26.7%	Pred. No. 9.1e-25;		
Matches 103;	Conservative 57;	Mismatches 131;	Indels 95;	Gaps 15;
QY	49	KSRTEAIKIQILSKLRLEQAPNISRDVIKQLLPKAPPLQELIDQYDVRDSSDGLSD	108	
DB	42	KKRIETAIRGQILSKLRASPQGE-----VPPGPLEAVLALYNSTRDVRAGESASP	95	
QY	109	D-----DYHATTET-IITMPTESDPLVQMEGKCCFFKPFSSKIOYKVVVQAQLWYL--	160	
DB	96	EPEPEADYIAKEVTVLVMTVETHNEI-----YDFKQSTHSIYMPF	135	
QY	161	-----RVQKPTTVFVQILRLIKPMK-----DGTRYTGIRSLKLDMPNG	199	
DB	136	NTSELREAVPEPVLSSRAELRLRLKLVKEQHVLYQKYSNNSWRYLSNRLAPSDSPE	195	
QY	200	TGIWQSIVKTVLQNLKQ-----PSNLGIEIKAPENGR-DLAVTF	241	
DB	196	-----MLSFDTGVVVRQWLRSRGSEIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDUATI-	251	
QY	242	PCPGEDGLN-PELEVRVTDTPK-----RSRRDFGLDCDEHSTESRCRYPLTVDF-BA	292	
DB	252	-----HGMNRPPILLMATPLERAQHLQSRHRRALDNYCFSTENKCCVRQLYIDFRKD	306	
QY	293	FGWDWIIAPKRYKANYCSGCECFVFLQYPHTH---LVHQANPRGSAGPCCTFTTKMSPN	349	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-18
Perfect score: 2014
Sequence: 1 MOKLAVYVYILFMQILVHP.....KEQIIYGKIPAMVVDRCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2014	100.0	375	3	US-09-859-211-27 Sequence 27, Appl
2	2014	100.0	375	3	US-09-841-730-18 Sequence 18, Appl
3	2014	100.0	375	3	US-09-872-856-27 Sequence 27, Appl
4	2014	100.0	375	4	US-10-463-973-27 Sequence 27, Appl
5	2014	100.0	375	4	US-10-456-852-14 Sequence 14, Appl
6	2003	99.5	375	4	US-10-074-152-35 Sequence 35, Appl
7	1994	99.0	375	3	US-09-859-211-23 Sequence 23, Appl
8	1994	99.0	375	3	US-09-872-856-23 Sequence 23, Appl
9	1994	99.0	375	4	US-10-463-973-23 Sequence 23, Appl
10	1994	99.0	375	4	US-10-456-852-10 Sequence 10, Appl
11	1994	99.0	375	4	US-10-662-438-6 Sequence 6, Appl
12	1994	99.0	375	5	US-10-665-374-6 Sequence 6, Appl
13	1991	98.9	375	4	US-10-074-152-34 Sequence 34, Appl
14	1989	98.8	374	3	US-09-841-730-8 Sequence 8, Appl
15	1984	98.5	375	4	US-10-278-803-27 Sequence 27, Appl
16	1964	97.5	375	4	US-10-278-803-23 Sequence 23, Appl
17	1871	92.9	375	3	US-09-454-540-5 Sequence 5, Appl
18	1871	92.9	375	3	US-09-859-211-14 Sequence 14, Appl
19	1871	92.9	375	3	US-09-841-730-2 Sequence 2, Appl
20	1871	92.9	375	3	US-09-872-856-14 Sequence 14, Appl
21	1871	92.9	375	3	US-09-871-604-5 Sequence 5, Appl
22	1871	92.9	375	4	US-10-074-152-29 Sequence 29, Appl
23	1871	92.9	375	4	US-10-278-803-14 Sequence 14, Appl
24	1871	92.9	375	4	US-10-071-499A-1 Sequence 1, Appl
25	1871	92.9	375	4	US-10-335-483-14 Sequence 14, Appl
26	1871	92.9	375	4	US-10-251-115-8 Sequence 8, Appl
27	1871	92.9	375	4	US-10-253-532-130 Sequence 130, App

ALIGNMENTS

RESULT 1

US-09-859-211-27
; Sequence 27, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-859-211-27

Query Match	100.0%;	Score	2014;	DB	3;	Length	375;
Best Local Similarity	100.0%;	Pred. No.	2.4e-181;				
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Qy	1	MOKLAVYVYILFMQILVHPVALDGS	QPTENA	KDGLNACTW	RQNTKSSR	IEAIKIQI	60

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-18
Perfect score: 2014
Sequence: 1 MOKLAVYVYVILFMQILVHP.....KEQIIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/aaa/6 COMB.pep.*
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4: /cgn2_6/ptodata/1/aaa/PCUS COMB.pep.*
5: /cgn2_6/ptodata/1/aaa/RE COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2014	100.0	375	2	US-09-686-344-27 Sequence 27, Appl
2	2014	100.0	375	2	US-09-626-896-18 Sequence 18, Appl
3	2014	100.0	375	2	US-09-485-046-14 Sequence 14, Appl
4	2014	100.0	375	2	US-09-841-730-18 Sequence 18, Appl
5	2003	99.5	375	2	US-09-252-149B-35 Sequence 35, Appl
6	1994	99.0	375	2	US-09-686-344-23 Sequence 23, Appl
7	1994	99.0	375	2	US-09-485-046-10 Sequence 34, Appl
8	1991	98.9	375	2	US-09-252-149B-34 Sequence 34, Appl
9	1989	98.8	374	2	US-09-626-896-8 Sequence 8, Appl
10	1989	98.8	374	2	US-09-841-730-8 Sequence 27, Appl
11	1984	98.5	375	2	US-09-451-501-27 Sequence 27, Appl
12	1984	98.5	375	2	US-10-278-803-27 Sequence 23, Appl
13	1964	97.5	375	2	US-09-451-501-23 Sequence 10, Appl
14	1964	97.5	375	2	US-10-278-803-23 Sequence 14, Appl
15	1871	92.9	375	1	US-08-525-596B-14 Sequence 5, Appl
16	1871	92.9	375	1	US-08-765-875-5 Sequence 5, Appl
17	1871	92.9	375	2	US-08-795-671-5 Sequence 14, Appl
18	1871	92.9	375	2	US-09-177-860A-14 Sequence 29, Appl
19	1871	92.9	375	2	US-09-252-149B-29 Sequence 14, Appl
20	1871	92.9	375	2	US-09-378-238-14 Sequence 14, Appl
21	1871	92.9	375	2	US-09-451-501-14 Sequence 5, Appl
22	1871	92.9	375	2	US-09-629-938-14 Sequence 14, Appl
23	1871	92.9	375	2	US-09-454-540-5 Sequence 2, Appl
24	1871	92.9	375	2	US-09-686-344-14 Sequence 2, Appl
25	1871	92.9	375	2	US-09-626-896-2 Sequence 4, Appl
26	1871	92.9	375	2	US-09-485-046-4 Sequence 14, Appl
27	1871	92.9	375	2	US-10-278-803-14 Sequence 14, Appl

28	1871	92.9	375	2	US-09-841-730-2	Sequence 2, Appl
29	1866	92.7	375	2	US-09-686-344-29	Sequence 29, Appl
30	1866	92.7	375	2	US-09-626-896-14	Sequence 14, Appl
31	1866	92.7	375	2	US-09-841-730-14	Sequence 14, Appl
32	1863	92.5	375	2	US-09-252-149B-32	Sequence 32, Appl
33	1862	92.5	375	2	US-09-451-501-19	Sequence 19, Appl
34	1862	92.5	375	2	US-10-278-803-19	Sequence 19, Appl
35	1861	92.4	375	2	US-09-252-149B-30	Sequence 30, Appl
36	1861	92.4	375	2	US-09-686-344-19	Sequence 19, Appl
37	1861	92.4	375	2	US-09-626-896-10	Sequence 10, Appl
38	1861	92.4	375	2	US-09-485-046-6	Sequence 6, Appl
39	1861	92.4	375	2	US-09-841-730-10	Sequence 10, Appl
40	1847	91.7	376	1	US-08-525-596B-12	Sequence 12, Appl
41	1847	91.7	376	2	US-09-177-860A-12	Sequence 12, Appl
42	1847	91.7	376	2	US-08-891-789B-6	Sequence 6, Appl
43	1847	91.7	376	2	US-09-252-149B-27	Sequence 27, Appl
44	1847	91.7	376	2	US-09-378-238-12	Sequence 12, Appl
45	1847	91.7	376	2	US-09-451-501-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-686-344-27
; Sequence 27, Application US/09686344
; Patent No. 6607884
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/686,344
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 375
; TYPE: PRM
; ORGANISM: Meleagris gallopavo
US-09-686-344-27

Query Match 100.0%; Score 2014; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MOKLAVYVYVILFMQILVHPVALDSSQPTENAEXKGLCNACTWRONTKSSRIEAIKIQI	60
Db	1	MOKLAVYVYVILFMQILVHPVALDSSQPTENAEXKGLCNACTWRONTKSSRIEAIKIQI	60
Qy	61	LSKLEAPNISRDVIKQLLPKAPPLQELIDQYDVRDSDSGSLEDDDYHATTETIIT	120
Db	61	LSKLEAPNISRDVIKQLLPKAPPLQELIDQYDVRDSDSGSLEDDDYHATTETIIT	120
Qy	121	MPTESDFLVQMEGKPKCCFFKFSKIQNKVKAOLWYLRQVKPTTVFVILRIKPM	180
Db	121	MPTESDFLVQMEGKPKCCFFKFSKIQNKVKAOLWYLRQVKPTTVFVILRIKPM	180
Qy	181	KDGTTRYTGIRSLKLDMMNFGTGIWQSIDVKTVLQNLWKQPESNLGIEIKAFDNGRDLAVT	240
Db	181	KDGTTRYTGIRSLKLDMMNFGTGIWQSIDVKTVLQNLWKQPESNLGIEIKAFDNGRDLAVT	240

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-16

Perfect score: 2011

Sequence: 1 MQLQIFVYIYLFMLVAGP.....KEQIIVKIPGMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
- 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	250	12.9	431	1	US-10-816-768-39
3	246	12.2	429	1	US-10-967-457-74
4	245.5	12.2	366	7	US-11-091-334-9
5	238.5	11.9	364	1	US-10-131-826A-342
6	238.5	11.9	364	7	US-11-091-334-2
7	230.5	11.5	102	1	US-10-816-768-47
8	223.5	11.1	102	1	US-10-816-768-53
9	222.5	11.1	102	1	US-10-816-768-46
10	221.5	11.0	102	1	US-10-816-768-100
11	220.5	11.0	129	1	US-10-816-768-89
12	220	10.9	139	1	US-10-816-768-68
13	218.5	10.9	117	1	US-10-816-768-69
14	214.5	10.7	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-55
16	212.5	10.6	102	1	US-10-816-768-86
17	212.5	10.6	102	1	US-10-816-768-88
18	211.5	10.5	102	1	US-10-816-768-84
19	211	10.5	101	1	US-10-816-768-59
20	207.5	10.3	106	1	US-10-816-768-62
21	207.5	10.3	106	1	US-10-816-768-63
22	207	10.3	101	1	US-10-816-768-49
23	206.5	10.3	102	1	US-10-816-768-83
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25	205.5	10.2	102	1	US-10-816-768-52

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1

; GENERAL INFORMATION:

; APPLICANT: RIKEN

; APPLICANT: KABUSHIKI KAISHA DANAFORM

; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336 (PCT)

; CURRENT APPLICATION NUMBER: US/10/517,544

; CURRENT FILING DATE: 2004-12-10

; PRIOR APPLICATION NUMBER: JP 2002-171851

; PRIOR FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: JP 2002-235294

; PRIOR FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 77

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-517-544-77

Query Match	15.5%	Score 312.5;	DB 1;	Length 391;
Best Local Similarity	27.6%	Pred No. 3.1e-24;		
Matches	102;	Conservative 61;	Mismatches 145;	Indels 61;
Gaps	15;			
QY	49	KSSLEAIKIQILSKRLLETAPNISKAIRQLLPKAPPLRELIDQYDVORDSDSGSLED	108	
DB	42	KKKRIEAIKQILSKRLASPPSQGE-----VPPGPLEAVLALYNSTRDRVAGSAEP	95	
QY	109	D-----DYHTTET-VITMPTESDLAEVQEKPCFFKFFSKIQNKV-----VKAQL	156	
DB	96	EPEEADYAKETRLVMVETHEIYDKFQSTHSIYMPFNTSELREAVPEPVLGRAEL	155	
QY	157	WYLRPVKPTTTFVQILRLIKPMKDGTRYTGIRSLKIDMNPCTGIWQSIDVKTQLQNWL	216	
DB	156	RL-LRRLKLVQEHVELYQ-----KYSNNSWRYLNRLLAPSDSPF---WLSFDVTGVVRQWL	209	
QY	217	KQPSNLGIEIKA-----LDENGH-----DLAVTFPPEGEGLN-PFLEVKV	257	
DB	210	SRGGIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDLATI-----HGMNRPFLLLMA	263	
QY	258	TUTPK-----RSRRDFGLDCDEHSTSRCCRYPLTVDF-BAFGWDWIIAPRYANYC	309	
DB	264	TLERAQHLQSSRRRALDNTNYCFSSTEKNCVQRLYIDFRKDLGKWKIHEPKGYHANFC	323	
QY	310	SGECFFLQKYPHPTH---LVHQNPKSGAGCCTPTKMSPINMLYFNGKEIYVKIPG	366	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-16

Perfect score: 2011

Sequence: 1 MOKLQIFVYIYLFMLLVAGP.....KEQIIYKIGKVMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2011	100.0	375	3	US-09-859-211-31
2	2011	100.0	375	3	US-09-841-730-16
3	2011	100.0	375	3	US-09-872-856-31
4	2011	100.0	375	4	US-10-463-973-31
5	2008	99.9	375	4	US-10-074-152-33
6	1943	96.6	375	3	US-09-859-211-29
7	1943	96.6	375	3	US-09-841-730-14
8	1943	96.6	375	3	US-09-872-856-29
9	1943	96.6	375	4	US-10-463-973-29
10	1940	96.5	375	4	US-10-074-152-32
11	1917	95.3	375	3	US-09-454-540-5
12	1917	95.3	375	3	US-09-859-211-14
13	1917	95.3	375	3	US-09-841-730-2
14	1917	95.3	375	3	US-09-872-856-14
15	1917	95.3	375	3	US-09-871-604-5
16	1917	95.3	375	4	US-10-074-152-29
17	1917	95.3	375	4	US-10-278-803-14
18	1917	95.3	375	4	US-10-071-499A-1
19	1917	95.3	375	4	US-10-335-483-14
20	1917	95.3	375	4	US-10-251-115-8
21	1917	95.3	375	4	US-10-253-532-130
22	1917	95.3	375	4	US-10-366-345-51
23	1917	95.3	375	4	US-10-463-973-14
24	1917	95.3	375	4	US-10-456-852-4
25	1917	95.3	375	4	US-10-459-127-5
26	1917	95.3	375	4	US-10-662-438-2
27	1917	95.3	375	5	US-10-689-677C-2

28	1917	95.3	375	5	US-10-665-374-2	Sequence 2, Appl
29	1917	95.3	375	5	US-10-997-809-14	Sequence 14, Appl
30	1917	95.3	375	5	US-10-991-343-14	Sequence 14, Appl
31	1917	95.3	375	6	US-11-019-001-1	Sequence 1, Appl
32	1917	95.3	376	3	US-09-813-398-38	Sequence 38, Appl
33	1917	95.3	376	5	US-10-826-324-38	Sequence 18, Appl
34	1916	95.3	375	4	US-10-278-803-19	Sequence 19, Appl
35	1915	95.2	375	3	US-09-859-211-19	Sequence 19, Appl
36	1915	95.2	375	3	US-09-841-730-10	Sequence 19, Appl
37	1915	95.2	375	3	US-09-872-856-19	Sequence 19, Appl
38	1915	95.2	375	4	US-10-074-152-30	Sequence 30, Appl
39	1915	95.2	375	4	US-10-463-973-19	Sequence 19, Appl
40	1915	95.2	375	4	US-10-456-852-6	Sequence 6, Appl
41	1912	95.1	375	3	US-09-859-894A-5	Sequence 5, Appl
42	1892	94.1	375	4	US-10-278-803-21	Sequence 21, Appl
43	1890	94.0	375	3	US-09-859-211-21	Sequence 21, Appl
44	1890	94.0	375	3	US-09-841-730-12	Sequence 12, Appl
45	1890	94.0	375	3	US-09-872-856-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-31
; Sequence 31, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Ovine
US-09-859-211-31

Query Match	100.0%	Score	2011;	DB	3;	Length	375;
Best Local Similarity	100.0%	Pred. No.	2.7e-180;				
Matches	375;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MOKLQIFVYIYLFMLLVAGPVDLNENSEKENVKGLCNACLRWQNNKSRLEAIKIQI	60				
Db	1	MOKLQIFVYIYLFMLLVAGPVDLNENSEKENVKGLCNACLRWQNNKSRLEAIKIQI	60				
Qy	61	LSKRLRLETAFNISKDAIRQLLPKAPPLRELIQYDVQDDSDSGSLEDDEDDYHVTETVIT	120				
Db	61	LSKRLRLETAFNISKDAIRQLLPKAPPLRELIQYDVQDDSDSGSLEDDEDDYHVTETVIT	120				
Qy	121	MPTESDLLAEVQSKPKCCPFKFSKIOHNVKAQMIYLRPVKTPPTVFQIILKPM	180				
Db	121	MPTESDLLAEVQSKPKCCPFKFSKIOHNVKAQMIYLRPVKTPPTVFQIILKPM	180				
Qy	181	KDGRYTGIRSLKLDMMNPGTGIWQSIDKVTVLQNLWKPESNLGIEIKALDENGHLAVT	240				

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 19.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-16

Perfect score: 2011

Sequence: 1 MOKLQIFVYIYLFMLLVAGP.....KEQIIYKIPGMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2011	100.0	375	2	US-09-686-344-31
2	2011	100.0	375	2	US-09-626-896-16
3	2011	100.0	375	2	US-09-841-730-10
4	2008	99.9	375	2	US-09-252-1498-33
5	1943	96.6	375	2	US-09-686-344-29
6	1943	96.6	375	2	US-09-626-896-14
7	1943	96.6	375	2	US-09-841-730-14
8	1940	96.5	375	2	US-09-252-1498-32
9	1917	95.3	375	1	US-08-525-596B-14
10	1917	95.3	375	1	US-08-765-875-5
11	1917	95.3	375	2	US-08-795-671-5
12	1917	95.3	375	2	US-09-177-860A-14
13	1917	95.3	375	2	US-09-252-1498-29
14	1917	95.3	375	2	US-09-378-238-14
15	1917	95.3	375	2	US-09-451-501-14
16	1917	95.3	375	2	US-09-629-938-14
17	1917	95.3	375	2	US-09-454-540-5
18	1917	95.3	375	2	US-09-686-344-14
19	1917	95.3	375	2	US-09-626-896-2
20	1917	95.3	375	2	US-09-485-046-4
21	1917	95.3	375	2	US-10-278-803-14
22	1917	95.3	375	2	US-09-841-730-2
23	1916	95.3	375	2	US-09-451-501-19
24	1916	95.3	375	2	US-10-278-803-19
25	1915	95.2	375	2	US-09-252-1498-30
26	1915	95.2	375	2	US-09-686-344-19
27	1915	95.2	375	2	US-09-626-896-10

28	1915	95.2	375	2	US-09-485-046-6	Sequence 6, Appl
29	1915	95.2	375	2	US-09-841-730-10	Sequence 10, Appl
30	1892	94.1	375	2	US-09-451-501-21	Sequence 21, Appl
31	1892	94.1	375	2	US-10-278-803-21	Sequence 21, Appl
32	1890	94.0	375	2	US-08-891-789B-2	Sequence 2, Appl
33	1890	94.0	375	2	US-09-686-344-21	Sequence 21, Appl
34	1890	94.0	375	2	US-09-626-896-12	Sequence 12, Appl
35	1890	94.0	375	2	US-09-485-046-8	Sequence 8, Appl
36	1890	94.0	375	2	US-09-841-730-12	Sequence 12, Appl
37	1890	94.0	376	1	US-08-525-596B-12	Sequence 12, Appl
38	1890	94.0	376	2	US-09-177-860A-12	Sequence 12, Appl
39	1890	94.0	376	2	US-08-891-789B-6	Sequence 6, Appl
40	1890	94.0	376	2	US-09-252-1498-27	Sequence 27, Appl
41	1890	94.0	376	2	US-09-378-238-12	Sequence 12, Appl
42	1890	94.0	376	2	US-09-451-501-12	Sequence 12, Appl
43	1890	94.0	376	2	US-09-629-938-12	Sequence 12, Appl
44	1890	94.0	376	2	US-09-686-344-12	Sequence 12, Appl
45	1890	94.0	376	2	US-09-626-896-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-686-344-31
; Sequence 31, Application US/09686344
; Patent No. 6607884
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/686,344
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Ovine
US-09-686-344-31

Query Match		100.0%	Score 2011;	DB 2;	Length 375;
Best Local Similarity		100.0%	Pred. No. 4.2e-185;		
Matches		375;	Conservative	0;	Mismatches
				Indels	Gaps
				0;	0;
QY	1	MOKLQIFVYIYLFMLLVAGPVDLNENSQKENVKKGKLCNACLMFQNNKSSRLBAIKIQI	60		
Db	1	MOKLQIFVYIYLFMLLVAGPVDLNENSQKENVKKGKLCNACLMFQNNKSSRLBAIKIQI	60		
QY	61	LSKRLTAPNISKDAIRQLPKAPPLRELDDQVDDSDSGSLEDHVVHTTETVIT	120		
Db	61	LSKRLTAPNISKDAIRQLPKAPPLRELDDQVDDSDSGSLEDHVVHTTETVIT	120		
QY	121	MPTESDLIAEVOEKPKCCFFKSSKIQHNKVVAQWLWYLRPVKTPPTTVFQILRLIKPM	180		
Db	121	MPTESDLIAEVOEKPKCCFFKSSKIQHNKVVAQWLWYLRPVKTPPTTVFQILRLIKPM	180		
QY	181	KDGRYTGIRSLKLDMPFGTGIWQSIDVKTVLQNLWKQPESNLGIKALDENGHDVAVT	240		
Db	181	KDGRYTGIRSLKLDMPFGTGIWQSIDVKTVLQNLWKQPESNLGIKALDENGHDVAVT	240		

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-14

Perfect score: 2013

Sequence: 1 MQLQIVYVILFMLIVAGP.....KEQIIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308.5	15.3	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	236.5	11.7	366	7	US-11-091-334-9
4	233	11.6	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.4	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.9	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	217.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.1	102	1	US-10-816-768-87
27	199.5	9.9	98	1	US-10-816-768-41
28	199.5	9.9	98	1	US-10-816-768-42
29	193	9.6	103	1	US-10-816-768-50
30	192	9.5	101	1	US-10-816-768-51
31	190.5	9.5	102	1	US-10-816-768-45
32	189.5	9.4	98	1	US-10-816-768-44
33	188.5	9.4	98	1	US-10-816-768-43
34	187	9.3	107	1	US-10-816-768-58
35	181.5	9.0	98	1	US-10-816-768-40
36	180	8.9	103	1	US-10-816-768-54
37	178.5	8.9	98	1	US-10-816-768-64
38	176	8.7	35	1	US-10-816-768-9
39	174.5	8.7	118	1	US-10-816-768-48
40	173.5	8.6	102	1	US-10-816-768-57
41	142.5	7.1	102	1	US-10-816-768-60
42	124.5	6.2	104	1	US-10-816-768-65
43	111	5.5	39	1	US-10-816-768-115
44	109	5.4	39	1	US-10-816-768-119
45	109	5.4	39	1	US-10-816-768-120

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KANISHIKI KAJISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.3%	Score 308.5; DB 1; Length 391;
Best Local Similarity	26.7%	Pred. No. 2.1e-24;
Matches 103; Conservative	57; Mismatches 131; Indels	95; Gaps 15;
QY	49	KSSRLKAIKIQILSKRLKLEAPNISKDAIRQLPKAPPLRELIDQYVORDSSDGSLED 108
DB	42	KRKRIEIRGQILSKRLASPPSQE-----VPPGPLEAVLALYNSRDRVAGESAEP 95
QY	109	D-----DYHATET-IITMPESDLMLQVEGKPKCCFKFSKIQYKNVKAQLWYL-- 160
DB	96	EPPEADYAKVETRVLMVETHNEI-----YDKFKSTHGIYMPF 135
QY	161	-----RVKTPTVFVQILRLIKPMK-----DGTRYTGIRSLKLDMPG 199
DB	136	NTSELRVAVPVLVLSRAELRLRLKLVQHVHLYOKYNNWRYLSNRLLASDSFE 195
QY	200	TGIWQSIDVKTVLQNLWKQPSNLGIEIKA-----LDENGH-----DLAVTF 241
DB	196	---WLSFDVTGVVQWLSRGGEIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDLATI- 251
QY	242	PGGEDGLN-PFLEVKVYTDTPK-----RRRRDFGLDCDEHSTESRCRPLTVDF-EA 292
DB	252	-----HGNRPFLLIMATPLERAQHLQSSRRHRLDNTNYCFSTKNCNCCVQLYIDFRK 306
QY	293	FGMDWIIAPKRYKANYCSGCECFVLOKYPHTH---LVHQANPRGSAGPCCTPTTQMSPIN 349

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-14

Perfect score: 2013

Sequence: 1 MQLQIYVYIYLFMLIVAGP.....KEQIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	2013	100.0	375	3 US-09-859-211-29
2	2013	100.0	375	3 US-09-841-730-14
3	2013	100.0	375	3 US-09-872-856-29
4	2013	100.0	375	4 US-10-463-973-29
5	2010	99.9	375	4 US-10-074-152-32
6	1979	98.3	375	3 US-09-454-540-5
7	1979	98.3	375	3 US-09-859-211-14
8	1979	98.3	375	3 US-09-841-730-2
9	1979	98.3	375	3 US-09-872-856-14
10	1979	98.3	375	3 US-09-871-604-5
11	1979	98.3	375	4 US-10-074-152-29
12	1979	98.3	375	4 US-10-278-803-14
13	1979	98.3	375	4 US-10-071-499A-1
14	1979	98.3	375	4 US-10-335-483-14
15	1979	98.3	375	4 US-10-251-115-8
16	1979	98.3	375	4 US-10-253-532-130
17	1979	98.3	375	4 US-10-366-345-51
18	1979	98.3	375	4 US-10-463-973-14
19	1979	98.3	375	4 US-10-456-852-4
20	1979	98.3	375	4 US-10-459-127-5
21	1979	98.3	375	4 US-10-662-438-2
22	1979	98.3	375	5 US-10-689-677C-2
23	1979	98.3	375	5 US-10-665-374-2
24	1979	98.3	375	5 US-10-997-809-14
25	1979	98.3	375	5 US-10-991-343-14
26	1979	98.3	375	6 US-11-019-001-1
27	1979	98.3	376	3 US-09-813-398-38

28	1979	98.3	376	5 US-10-826-324-38	Sequence 38, Appl
29	1978	98.3	375	4 US-10-278-803-19	Sequence 19, Appl
30	1977	98.2	375	3 US-09-859-211-19	Sequence 19, Appl
31	1977	98.2	375	3 US-09-841-730-10	Sequence 10, Appl
32	1977	98.2	375	3 US-09-872-856-19	Sequence 19, Appl
33	1977	98.2	375	4 US-10-074-152-30	Sequence 30, Appl
34	1977	98.2	375	4 US-10-463-973-19	Sequence 19, Appl
35	1977	98.2	375	4 US-10-456-852-6	Sequence 6, Appl
36	1974	98.1	375	3 US-09-859-894A-5	Sequence 5, Appl
37	1956	97.2	376	3 US-09-859-894A-11	Sequence 11, Appl
38	1956	97.2	376	3 US-09-859-211-12	Sequence 12, Appl
39	1956	97.2	376	3 US-09-841-730-4	Sequence 4, Appl
40	1956	97.2	376	3 US-09-872-856-12	Sequence 12, Appl
41	1956	97.2	376	3 US-09-871-604-10	Sequence 10, Appl
42	1956	97.2	376	4 US-10-074-152-27	Sequence 27, Appl
43	1956	97.2	376	4 US-10-278-803-12	Sequence 12, Appl
44	1956	97.2	376	4 US-10-335-483-12	Sequence 12, Appl
45	1956	97.2	376	4 US-10-251-115-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-29
; Sequence 29, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Porcine
US-09-859-211-29

Query Match 100.0%; Score 2013; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.1e-183;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQLQIYVYIYLFMLIVAGPVDLNENSEKENVKEGLCNACMRONTKSSRLRAIKQI	60
Db	1	MQLQIYVYIYLFMLIVAGPVDLNENSEKENVKEGLCNACMRONTKSSRLRAIKQI	60
Qy	61	LSKRLLETAPNISKDAIRQLLPKAPPLRELIDQYDVRDDSDSGSLEDDEDDYHATTETIT	120
Db	61	LSKRLLETAPNISKDAIRQLLPKAPPLRELIDQYDVRDDSDSGSLEDDEDDYHATTETIT	120
Qy	121	MPTESDILLMQVEGPKCCFFKFSKSIQNKVKVQAQLWYLRPVKTPTTVFVQILRLIKPM	180
Db	121	MPTESDILLMQVEGPKCCFFKFSKSIQNKVKVQAQLWYLRPVKTPTTVFVQILRLIKPM	180
Qy	181	KDGTFTYTGIRSLKLDMPGTCGIWQSIDVKTVQLNWLKQPESNLGIEIKALDENGHLAVT	240

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-14

Perfect score: 2013

Sequence: 1 MQKLQIYVYIYLFMLIVAGP.....KEQIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2013	100.0	375	2	US-09-686-344-29
2	2013	100.0	375	2	US-09-626-896-14
3	2013	100.0	375	2	US-09-841-730-14
4	2010	99.9	375	2	US-09-252-149B-32
5	1979	98.3	375	1	US-08-525-596B-14
6	1979	98.3	375	1	US-08-785-875-5
7	1979	98.3	375	2	US-08-795-671-5
8	1979	98.3	375	2	US-09-177-860A-14
9	1979	98.3	375	2	US-09-252-149B-29
10	1979	98.3	375	2	US-09-378-238-14
11	1979	98.3	375	2	US-09-451-501-14
12	1979	98.3	375	2	US-09-629-938-14
13	1979	98.3	375	2	US-09-454-540-5
14	1979	98.3	375	2	US-09-686-344-14
15	1979	98.3	375	2	US-09-626-896-2
16	1979	98.3	375	2	US-09-485-046-4
17	1979	98.3	375	2	US-10-278-803-14
18	1979	98.3	375	2	US-09-841-730-2
19	1978	98.3	375	2	US-09-451-501-19
20	1978	98.3	375	2	US-10-278-803-19
21	1977	98.2	375	2	US-09-252-149B-30
22	1977	98.2	375	2	US-09-686-344-19
23	1977	98.2	375	2	US-09-626-896-10
24	1977	98.2	375	2	US-09-485-046-6
25	1977	98.2	375	2	US-09-841-730-10
26	1956	97.2	376	1	US-08-525-596B-12
27	1956	97.2	376	2	US-09-177-860A-12

28	1956	97.2	376	2	US-08-891-789B-6	Sequence 6, Appl
29	1956	97.2	376	2	US-09-252-149B-27	Sequence 27, Appl
30	1956	97.2	376	2	US-09-378-238-12	Sequence 12, Appl
31	1956	97.2	376	2	US-09-451-501-12	Sequence 12, Appl
32	1956	97.2	376	2	US-09-629-938-12	Sequence 12, Appl
33	1956	97.2	376	2	US-09-686-344-12	Sequence 12, Appl
34	1956	97.2	376	2	US-09-626-896-4	Sequence 4, Appl
35	1956	97.2	376	2	US-09-485-046-2	Sequence 2, Appl
36	1956	97.2	376	2	US-10-278-803-12	Sequence 12, Appl
37	1956	97.2	376	2	US-09-841-730-4	Sequence 4, Appl
38	1943	96.5	375	2	US-09-686-344-31	Sequence 31, Appl
39	1943	96.5	375	2	US-09-626-896-16	Sequence 16, Appl
40	1943	96.5	375	2	US-09-841-730-16	Sequence 16, Appl
41	1940	96.4	375	2	US-09-252-149B-33	Sequence 33, Appl
42	1929	95.8	375	2	US-09-451-501-21	Sequence 21, Appl
43	1929	95.8	375	2	US-10-278-803-21	Sequence 21, Appl
44	1928	95.8	376	2	US-09-252-149B-28	Sequence 28, Appl
45	1928	95.8	376	2	US-09-451-501-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-686-344-29

; Sequence 29, Application US/09686344

; Patent No. 6607884

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; APPLICANT: McPherson, Alexandra C.

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

; FILE REFERENCE: 07265/144001

; CURRENT APPLICATION NUMBER: US/09/686,344

; CURRENT FILING DATE: 2000-10-10

; PRIOR APPLICATION NUMBER: 08/862,445

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 08/847,910

; PRIOR FILING DATE: 1997-04-28

; PRIOR APPLICATION NUMBER: 08/795,071

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: 08/525,596

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: PCT/US94/03019

; PRIOR FILING DATE: 1994-03-18

; PRIOR APPLICATION NUMBER: 08/033,923

; PRIOR FILING DATE: 1993-03-19

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Porcine

US-09-686-344-29

Query Match

Best Local Similarity 100.0%; Score 2013; DB 2; Length 375;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVKEGLCNACMRQNTKSRLEAIKIQI	60
Db	1	MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVKEGLCNACMRQNTKSRLEAIKIQI	60
Qy	61	LSKLRLTAPNISKDAIRQLLPKAPPLRELIDQVDORDDSSDGSLEDDDHATTETIIT	120
Db	61	LSKLRLTAPNISKDAIRQLLPKAPPLRELIDQVDORDDSSDGSLEDDDHATTETIIT	120
Qy	121	MPTESDLLMVEGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKPTPTTVFVQILRLIKPM	180
Db	121	MPTESDLLMVEGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKPTPTTVFVQILRLIKPM	180
Qy	181	KDGFRYTGIRSLKLDNMPGTGIIWQSIDVKTVLQNLWKQPSNLGIRIKALDENGHDLA	240
Db	181	KDGFRYTGIRSLKLDNMPGTGIIWQSIDVKTVLQNLWKQPSNLGIRIKALDENGHDLA	240

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-12
Perfect score: 2003
Sequence: 1 MQLQISVVIYLFMLIVAGP.....EQIIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
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4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292.5	14.6	391	1	US-10-517-544-77
2	255	12.7	431	1	US-10-816-768-39
3	248.5	12.4	366	7	US-11-091-334-9
4	239.5	12.0	364	1	US-10-131-826A-342
5	239.5	12.0	364	7	US-11-091-334-2
6	228.5	11.4	102	1	US-10-816-768-47
7	225	11.2	429	1	US-10-967-457-74
8	221.5	11.1	102	1	US-10-816-768-53
9	219.5	11.0	129	1	US-10-816-768-89
10	219	10.9	139	1	US-10-816-768-68
11	218.5	10.9	203	1	US-10-816-768-100
12	217.5	10.8	117	1	US-10-816-768-69
13	216.5	10.8	102	1	US-10-816-768-46
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.5	102	1	US-10-816-768-84
18	209.5	10.5	102	1	US-10-816-768-88
19	208	10.4	101	1	US-10-816-768-59
20	203.5	10.2	102	1	US-10-816-768-52
21	203.5	10.2	102	1	US-10-816-768-56
22	203.5	10.2	102	1	US-10-816-768-83
23	202.5	10.1	102	1	US-10-816-768-87
24	202.5	10.1	106	1	US-10-816-768-62
25	202.5	10.1	106	1	US-10-816-768-63

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: KANUSHIKI KAISHA DANAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-517-544-77

Query Match	14.6%	Score 292.5;	DB 1;	Length 391;
Best Local Similarity	26.4%	Pred. No. 1.9e-23;		
Matches 101;	Conservative 56;	Mismatches 131;	Indels 95;	Gaps 15;
QY	52	RUEAIKIQILSKRLTETAPNISKDAIRQLLPKAPPLLELIDQFDVORDASSDGSLEDD--	109	
Db	45	RTEAIRGQILSKRLASPPSQGE-----VPPGPLEAVLALYNSTRDRVAGESAPSPPE	98	
QY	110	---DYHARTET-VITMPTIESDLTTQVEGKPKCCFFKFSKIQYNKLVAKQLMTYL-----	160	
Db	99	PEADYAYAKEVTVLMVETHEI-----YDKPKQTHSIYMFNTS	138	
QY	161	---RPVKPVPATVFVQILRLIKPMK-----DGTRYTGIRSLKLDMPGTGI	202	
Db	139	ELREAVPEVLLSRAELRLRLKLVQEHVELYQKYSNNRYLSNRLAPSDSP-----	195	
QY	203	WQSIDVKTVLQWNLKOPESNLGIEIKA-----LDENGH-----DLAVTFPEP	244	
Db	196	WLSFDVTGVVRQWLSRGGEIEGFRLSAHCSDSDNTLQWDINGFTTGRGDLATI-----	251	
QY	245	GEDGTLT-PLEVKVYTDTPK-----RSRRDFGLCDEHSTESRCRYPLTVDFP-SAFGW	295	
Db	252	--HGMNRPPLLMLATPFLERAQHLQSSRRHRLADNTYCFSSKNCNCCVRLYIDFRKDLGW	309	
QY	296	DWIIAPKRYKANYCSGECEFFVLQKYPHTH---LVHQANPRGSAGPCCTPTTKMSPINMLY	352	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-12

Perfect score: 2003

Sequence: 1 MQLQISVYIYLFMLIVAGP.....EQIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	100.0	375	3	US-09-859-211-21
2	2003	100.0	375	3	US-09-841-730-12
3	2003	100.0	375	3	US-09-872-856-21
4	2003	100.0	375	4	US-10-251-115-2
5	2003	100.0	375	4	US-10-463-973-21
6	2003	100.0	375	4	US-10-456-852-8
7	2003	100.0	375	5	US-10-662-438-4
8	2003	100.0	375	5	US-10-665-374-4
9	2000	99.9	375	4	US-10-074-152-31
10	1997	99.7	375	4	US-10-074-152-2
11	1973	98.5	375	4	US-10-278-803-21
12	1927	96.2	375	3	US-09-859-211-29
13	1927	96.2	375	3	US-09-841-730-14
14	1927	96.2	375	3	US-09-872-856-29
15	1927	96.2	375	4	US-10-463-973-29
16	1924	96.1	375	4	US-10-074-152-32
17	1906	95.2	375	3	US-09-454-540-5
18	1906	95.2	375	3	US-09-859-211-14
19	1906	95.2	375	3	US-09-841-730-2
20	1906	95.2	375	3	US-09-872-856-14
21	1906	95.2	375	3	US-09-871-604-5
22	1906	95.2	375	4	US-10-074-152-29
23	1906	95.2	375	4	US-10-278-803-14
24	1906	95.2	375	4	US-10-071-499A-1
25	1906	95.2	375	4	US-10-335-483-14
26	1906	95.2	375	4	US-10-251-115-8
27	1906	95.2	375	4	US-10-253-532-130

ALIGNMENTS

RESULT 1

US-09-859-211-21
; Sequence 21, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Bovine
US-09-859-211-21

Query Match 100.0%; Score 2003; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 1.9e-103; Indels 0; Gaps 0;
Matches 375; Conservative 0; Mismatches 0;

Qy	1	MQLQISVYIYLFMLIVAGPVDLNENSEKENVKEGLCNACLWRENTTSSRLAIIQI	60
Db	1	MQLQISVYIYLFMLIVAGPVDLNENSEKENVKEGLCNACLWRENTTSSRLAIIQI	60
Qy	61	LSKRLLETAPNISKDAIRQLLPKAPPLLELDQDFVQRDASDGSLEDDDYHARTETVT	120
Db	61	LSKRLLETAPNISKDAIRQLLPKAPPLLELDQDFVQRDASDGSLEDDDYHARTETVT	120
Qy	121	MPTESDLITQVEGPKCCFFKFSKIQYNKLVAQLMILYLPVKTPATVFOVLRLIKPM	180
Db	121	MPTESDLITQVEGPKCCFFKFSKIQYNKLVAQLMILYLPVKTPATVFOVLRLIKPM	180
Qy	181	KDGRYTGIRSLKLDMPNPGTGWQSIDVKTQLNWLKQPESNLGIEIKALDENGHDLA	240

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-12

Perfect score: 2003

Sequence: 1 MOKLQISVYIYFLMVLVAGP.....EGQIIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB pep:*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB pep:*
- 3: /cgn2_6/ptodata/1/iaa/H COMB pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	100.0	375	2	US-08-891-789B-2
2	2003	100.0	375	2	US-09-686-344-21
3	2003	100.0	375	2	US-09-626-896-12
4	2003	100.0	375	2	US-09-485-046-8
5	2003	100.0	375	2	US-09-841-730-12
6	2000	99.9	375	2	US-09-252-149B-31
7	1997	99.7	375	2	US-09-252-149B-2
8	1973	98.5	375	2	US-09-451-501-21
9	1973	98.5	375	2	US-10-278-803-21
10	1927	96.2	375	2	US-09-686-344-29
11	1927	96.2	375	2	US-09-626-896-14
12	1927	96.2	375	2	US-09-841-730-14
13	1924	96.1	375	2	US-09-252-149B-32
14	1906	95.2	375	1	US-08-525-596B-14
15	1906	95.2	375	1	US-08-765-875-5
16	1906	95.2	375	2	US-08-795-671-5
17	1906	95.2	375	2	US-09-177-860A-14
18	1906	95.2	375	2	US-09-252-149B-29
19	1906	95.2	375	2	US-09-378-238-14
20	1906	95.2	375	2	US-09-451-501-14
21	1906	95.2	375	2	US-09-629-938-14
22	1906	95.2	375	2	US-09-454-540-5
23	1906	95.2	375	2	US-09-686-344-14
24	1906	95.2	375	2	US-09-626-896-2
25	1906	95.2	375	2	US-09-485-046-4
26	1906	95.2	375	2	US-10-278-803-14
27	1906	95.2	375	2	US-09-841-730-2

28	1905	95.1	375	2	US-09-451-501-19	Sequence 19, Appl
29	1905	95.1	375	2	US-10-278-803-19	Sequence 19, Appl
30	1904	95.1	375	2	US-09-252-149B-30	Sequence 30, Appl
31	1904	95.1	375	2	US-09-686-344-19	Sequence 19, Appl
32	1904	95.1	375	2	US-09-626-896-10	Sequence 10, Appl
33	1904	95.1	375	2	US-09-485-046-6	Sequence 10, Appl
34	1904	95.1	375	2	US-09-841-730-10	Sequence 10, Appl
35	1890	94.4	375	2	US-09-686-344-31	Sequence 31, Appl
36	1890	94.4	375	2	US-09-626-896-16	Sequence 16, Appl
37	1890	94.4	375	2	US-09-841-730-16	Sequence 16, Appl
38	1887	94.2	375	2	US-09-252-149B-33	Sequence 33, Appl
39	1876	93.7	376	1	US-08-525-596B-12	Sequence 12, Appl
40	1876	93.7	376	2	US-09-177-860A-12	Sequence 12, Appl
41	1876	93.7	376	2	US-08-891-789B-6	Sequence 6, Appl
42	1876	93.7	376	2	US-09-252-149B-27	Sequence 27, Appl
43	1876	93.7	376	2	US-09-378-238-12	Sequence 12, Appl
44	1876	93.7	376	2	US-09-451-501-12	Sequence 12, Appl
45	1876	93.7	376	2	US-09-629-938-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-08-891-789B-2
; Sequence 2, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891.789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-891-789B-2

Query Match 100.0%; Score 2003; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MOKLQISVYIYFLMVLVAGPVDLNSSEKENVKEGICNACLWRENTTSSRLRAIKQI	60
Db	1	MOKLQISVYIYFLMVLVAGPVDLNSSEKENVKEGICNACLWRENTTSSRLRAIKQI	60
Qy	61	LSKRLLETAPNISKDAIRQLLPKAPPLLELDIQFDVORDASSDGSLEDDDYHARTTIVIT	120
Db	61	LSKRLLETAPNISKDAIRQLLPKAPPLLELDIQFDVORDASSDGSLEDDDYHARTTIVIT	120

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-10
Perfect score: 2016
Sequence: 1 MQLQLCVYIYFLMLVAGP.....KEQIIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.New.*
- 1: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
 - 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap.*
 - 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap.*
 - 4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pap.*
 - 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
 - 6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
 - 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pap.*
 - 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	260	12.9	431	1	US-10-816-768-39
3	242.5	12.0	366	7	US-11-091-334-9
4	236.5	11.7	364	1	US-10-131-826A-342
5	236.5	11.7	364	7	US-11-091-334-2
6	234	11.6	429	1	US-10-967-457-74
7	232.5	11.5	102	1	US-10-816-768-47
8	225.5	11.2	102	1	US-10-816-768-53
9	223.5	11.1	129	1	US-10-816-768-89
10	223	11.1	139	1	US-10-816-768-68
11	222.5	11.0	203	1	US-10-816-768-100
12	221.5	11.0	102	1	US-10-816-768-46
13	221.5	11.0	117	1	US-10-816-768-69
14	216.5	10.7	102	1	US-10-816-768-85
15	216.5	10.7	102	1	US-10-816-768-86
16	214.5	10.6	102	1	US-10-816-768-55
17	213.5	10.6	102	1	US-10-816-768-84
18	213.5	10.6	102	1	US-10-816-768-88
19	212	10.5	101	1	US-10-816-768-59
20	208.5	10.3	106	1	US-10-816-768-62
21	208.5	10.3	106	1	US-10-816-768-63
22	207.5	10.3	102	1	US-10-816-768-52
23	207.5	10.3	102	1	US-10-816-768-56
24	206.5	10.2	102	1	US-10-816-768-87
25	206	10.2	101	1	US-10-816-768-49

26	205.5	10.2	102	1	US-10-816-768-83	Sequence 83, Appl
27	203.5	10.1	98	1	US-10-816-768-41	Sequence 41, Appl
28	203.5	10.1	98	1	US-10-816-768-42	Sequence 42, Appl
29	195	9.7	103	1	US-10-816-768-50	Sequence 50, Appl
30	194	9.6	101	1	US-10-816-768-51	Sequence 51, Appl
31	193.5	9.6	98	1	US-10-816-768-44	Sequence 44, Appl
32	192.5	9.5	98	1	US-10-816-768-43	Sequence 43, Appl
33	192.5	9.5	102	1	US-10-816-768-45	Sequence 45, Appl
34	189	9.4	107	1	US-10-816-768-58	Sequence 58, Appl
35	185.5	9.2	98	1	US-10-816-768-40	Sequence 40, Appl
36	182.5	9.1	98	1	US-10-816-768-64	Sequence 64, Appl
37	182	9.0	103	1	US-10-816-768-54	Sequence 54, Appl
38	178.5	8.9	118	1	US-10-816-768-48	Sequence 48, Appl
39	177.5	8.8	102	1	US-10-816-768-57	Sequence 57, Appl
40	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
41	146.5	7.3	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	113	5.6	105	1	US-10-816-768-61	Sequence 61, Appl
44	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
45	109	5.4	39	1	US-10-816-768-119	Sequence 119, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.5%	Score 312.5	DB 1	Length 391
Best Local Similarity	27.2%	Pred. No. 3.3e-25		
Matches	105	Conservative 55	Mismatches 131	Indels 95
Gaps	15			
QY	49	KSRRTAKIKIQLSKRLTAPNISKDATRQLLPKAPPLRELIDQYDQVDDSDSDSLED	108	
Db	42	KKRRTAKIKIQLSKRLTAPNISKDATRQLLPKAPPLRELIDQYDQVDDSDSDSLED	95	
QY	109	D-----DYHATTET-IITWPTESDPLQVQDKPKCFKFFSKIQNKVKAQWLIVL--	160	
Db	96	EPEPEADYAKETRVRLMVETHNEI-----YDKFKQSTHSIYMPF	135	
QY	161	-----RPVETPTTFVQILRLIKPMK-----DGTRYTGIRSKLDNMPG	199	
Db	136	NTSELREAVPEPVLRLSLRAELRLRLKLVKEQHVLYQKYNNSWYLSNRLAPSDE	195	
QY	200	TGWSIDVKTVLQNLKQFESNLGIEIQA-----LDENGH-----DLAVTF	241	
Db	196	-----WLSFDVTGVVQWLRSRGIEGPRLSAHCSDSRDNTLQVDINGFTTGRGDLATI-	251	
QY	242	PGGEDGLN-PLEVKVVTDPK-----RSRRDFGLDCDEHSTESRCRCRYPLTVDF-BA	292	
Db	252	-----HGMVRPFLMLMATPLERAQHLQSSRRRALDNTYCFSGSTEKNCCVQRQYIYDFKD	306	
QY	293	LQWDMIIAPKRYKANYCSGCEBFVFLQKYPHTH---LVHQANPRGSAGPCCTPTKMSPIN	349	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-10

Perfect score: 2016

Sequence: 1 MOKLQLCVYIYLFMLIVAGP.....KEQIIYKIPAMVVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2016	100.0	375	3	US-09-859-211-19
2	2016	100.0	375	3	US-09-841-730-10
3	2016	100.0	375	3	US-09-872-856-19
4	2016	100.0	375	4	US-10-074-152-30
5	2016	100.0	375	4	US-10-463-973-19
6	2016	100.0	375	4	US-10-456-852-6
7	2008	99.6	375	3	US-09-454-540-5
8	2008	99.6	375	3	US-09-859-211-14
9	2008	99.6	375	3	US-09-841-730-2
10	2008	99.6	375	3	US-09-872-856-14
11	2008	99.6	375	3	US-09-871-604-5
12	2008	99.6	375	4	US-10-074-152-29
13	2008	99.6	375	4	US-10-278-803-14
14	2008	99.6	375	4	US-10-071-499A-1
15	2008	99.6	375	4	US-10-335-483-14
16	2008	99.6	375	4	US-10-251-115-8
17	2008	99.6	375	4	US-10-253-532-130
18	2008	99.6	375	4	US-10-366-345-51
19	2008	99.6	375	4	US-10-463-973-14
20	2008	99.6	375	4	US-10-456-852-4
21	2008	99.6	375	4	US-10-459-127-5
22	2008	99.6	375	4	US-10-662-438-2
23	2008	99.6	375	5	US-10-689-677C-2
24	2008	99.6	375	5	US-10-665-374-2
25	2008	99.6	375	5	US-10-997-809-14
26	2008	99.6	375	5	US-10-991-343-14
27	2008	99.6	375	6	US-11-019-001-1

28	2008	99.6	376	3	US-09-813-398-38	Sequence 38, Appl
29	2008	99.6	376	5	US-10-826-324-38	Sequence 38, Appl
30	2007	99.6	375	4	US-10-278-803-19	Sequence 19, Appl
31	2003	99.4	375	3	US-09-859-894A-5	Sequence 5, Appl
32	1977	98.1	375	3	US-09-859-211-29	Sequence 29, Appl
33	1977	98.1	375	3	US-09-841-730-14	Sequence 14, Appl
34	1977	98.1	375	3	US-09-872-856-29	Sequence 29, Appl
35	1977	98.1	375	4	US-10-463-973-29	Sequence 29, Appl
36	1974	97.9	375	4	US-10-074-152-32	Sequence 32, Appl
37	1951	96.8	376	3	US-09-859-894A-11	Sequence 11, Appl
38	1951	96.8	376	3	US-09-859-211-12	Sequence 12, Appl
39	1951	96.8	376	3	US-09-841-730-4	Sequence 4, Appl
40	1951	96.8	376	3	US-09-872-856-12	Sequence 12, Appl
41	1951	96.8	376	3	US-09-871-604-10	Sequence 10, Appl
42	1951	96.8	376	4	US-10-074-152-27	Sequence 27, Appl
43	1951	96.8	376	4	US-10-278-803-12	Sequence 12, Appl
44	1951	96.8	376	4	US-10-335-483-12	Sequence 12, Appl
45	1951	96.8	376	4	US-10-251-115-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-19
; Sequence 19, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Baboon
US-09-859-211-19

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Gaps	0;						
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Db	1	MOKLQLCVYIYLFMLIVAGPVDLNENSEKEKVEKGCNACTWRQNTKSSRIEAIKQI	60				
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Qy	181	KDGRYTGIRSLKLDMPNPGTGIWQSIDVKTIVQNLKQPSNLGIEIKALDENGHLAVT	240				

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.39627 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-8
Perfect score: 2006
Sequence: 1 QKLAIVYVYLFMQIAVDPV.....KEQIIYGIKIPAMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.5	15.7	391	1	US-10-517-544-77
2	255	12.7	431	1	US-10-816-768-39
3	237	11.8	429	1	US-10-967-457-74
4	235	11.7	364	1	US-10-131-826A-342
5	235	11.7	364	7	US-11-091-334-2
6	233.5	11.6	366	7	US-11-091-334-9
7	228.5	11.4	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.9	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.4	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.2	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KARUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.7%	Score 315.5;	DB 1;	Length 391;
Best Local Similarity	27.1%	Pred. No. 4.6e-25;		
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Qy	48	KSRIRIAIKTQILSKRLKLEQAPNISRVIKQLPKAPPLQELIDYQVQVRDSDSGSLED	107	
Db	42	KRKRIEAIKQILSKRLKSLASPPSQE-----VPPGLPEAVLALYNSTRDRVAGESAEP	95	
Qy	108	D-----DYHATTET-IITMPTESDFVQMEGPKCCCFKPSKIQYNKVKQAQLWYL--	159	
Db	96	EPEPEADYAKETRVLMVETHNEI-----YDKFKQSTHSIYMFP	135	
Qy	160	-----RQVQKPTTVFVQILRLIKPMK-----DGTRYTGIRSLKLDMPNG	198	
Db	136	NTSELREAVPEVLUSRAELRLRLKLUKVEOHVELYQKYSNNRWYLNRLLPADSDPE	195	
Qy	199	TCIMOSIDVKTVLQNLKQ-----PESNLGIEIKAFDETGR--DLAVT	239	
Db	196	---WLSFDVTGVVRQKLSRGGIEGFRLSAHCSDSDRNTLQVDINGP--TTGRGDLATI	251	
Qy	240	FPGPGEGLN--PFLEVRVTDTPK-----RBRDFGLDCDHSSTESRCRPLTVDFP-E	290	
Db	252	-----HGMNRPFLMLMATPLERAQHLQSSRRRALDNYCFSPSTKCNCCVRQLYDFRK	305	
Qy	291	AFGNDWIIAPKRYKANYCSGCECFVFLQKYPTH-----LVHQANPRGSAGPCCTPTTQMSPI	347	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.2229 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-8

Perfect score: 206

Sequence: 1 OKLAVYVYIYLFMQIAVDPV.....KEQIIYKIPAMVDRGCS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	206	100.0	374	3	US-09-841-730-8	Sequence 8, Appli
2	206	100.0	375	3	US-09-859-211-23	Sequence 23, Appli
3	206	100.0	375	3	US-09-872-856-23	Sequence 23, Appli
4	206	100.0	375	4	US-10-463-973-23	Sequence 2, Appli
5	206	100.0	375	4	US-10-456-852-10	Sequence 10, Appli
6	206	100.0	375	4	US-10-662-438-6	Sequence 6, Appli
7	206	100.0	375	5	US-10-665-374-6	Sequence 6, Appli
8	2003	99.9	375	4	US-10-074-152-34	Sequence 34, Appli
9	1989	99.2	375	3	US-09-859-211-27	Sequence 27, Appli
10	1989	99.2	375	3	US-09-841-730-18	Sequence 18, Appli
11	1989	99.2	375	3	US-09-872-856-27	Sequence 27, Appli
12	1989	99.2	375	4	US-10-463-973-27	Sequence 27, Appli
13	1989	99.2	375	4	US-10-456-852-14	Sequence 14, Appli
14	1978	98.6	375	4	US-10-074-152-35	Sequence 35, Appli
15	1976	98.5	375	4	US-10-278-803-23	Sequence 23, Appli
16	1959	97.7	375	4	US-10-278-803-27	Sequence 27, Appli
17	1860	92.7	375	3	US-09-454-540-5	Sequence 5, Appli
18	1860	92.7	375	3	US-09-859-211-14	Sequence 14, Appli
19	1860	92.7	375	3	US-09-841-730-2	Sequence 2, Appli
20	1860	92.7	375	3	US-09-872-856-14	Sequence 14, Appli
21	1860	92.7	375	3	US-09-871-604-5	Sequence 5, Appli
22	1860	92.7	375	4	US-10-074-152-29	Sequence 29, Appli
23	1860	92.7	375	4	US-10-278-803-14	Sequence 14, Appli
24	1860	92.7	375	4	US-10-071-499A-1	Sequence 1, Appli
25	1860	92.7	375	4	US-10-335-483-14	Sequence 14, Appli
26	1860	92.7	375	4	US-10-251-115-8	Sequence 8, Appli
27	1860	92.7	375	4	US-10-253-532-130	Sequence 130, App

28	1860	92.7	375	4	US-10-366-345-51	Sequence 51, Appli
29	1860	92.7	375	4	US-10-463-973-14	Sequence 14, Appli
30	1860	92.7	375	4	US-10-456-852-4	Sequence 4, Appli
31	1860	92.7	375	4	US-10-459-127-5	Sequence 5, Appli
32	1860	92.7	375	4	US-10-662-438-2	Sequence 2, Appli
33	1860	92.7	375	5	US-10-688-677C-2	Sequence 2, Appli
34	1860	92.7	375	5	US-10-665-374-2	Sequence 2, Appli
35	1860	92.7	375	5	US-10-997-809-14	Sequence 14, Appli
36	1860	92.7	375	5	US-10-991-343-14	Sequence 14, Appli
37	1860	92.7	375	6	US-11-019-001-1	Sequence 1, Appli
38	1860	92.7	376	3	US-09-813-398-38	Sequence 38, Appli
39	1860	92.7	376	5	US-10-826-324-38	Sequence 38, Appli
40	1855	92.5	375	3	US-09-859-894A-5	Sequence 5, Appli
41	1855	92.5	375	3	US-09-859-211-29	Sequence 29, Appli
42	1855	92.5	375	3	US-09-841-730-14	Sequence 14, Appli
43	1855	92.5	375	3	US-09-872-856-29	Sequence 29, Appli
44	1855	92.5	375	4	US-10-463-973-29	Sequence 29, Appli
45	1852	92.3	375	4	US-10-074-152-32	Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-09-841-730-8
; Sequence 8, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/155598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-841-730-8

Query Match	100.0%	Score 2066;	DB 3;	Length 374;
Best Local Similarity	100.0%;	Pred. No. 1.3e-180;	Mismatches 0;	Indels 0;
Matches 374;	Conservative	0;		Gaps 0;
Qy	1	OKLAVYVYIYLFMQIAVDPV	ALDGSSTENAEKGLCNACTWRONTKSSRIEAIKQIL	60
Db	1	OKLAVYVYIYLFMQIAVDPV	ALDGSSTENAEKGLCNACTWRONTKSSRIEAIKQIL	60
Qy	61	SKLRLEQAPNISRDVIKQLLPKAPPLQELIDQYDVQDRDSDGSLDDDDYHATTETITM	120	
Db	61	SKLRLEQAPNISRDVIKQLLPKAPPLQELIDQYDVQDRDSDGSLDDDDYHATTETITM	120	
Qy	121	PTESDFLVQMEGKPKCCFFKPFSSKIQYKVKVKAQIWLRYLQVOKPTTVFVQILRLIKPMK	180	
Db	121	PTESDFLVQMEGKPKCCFFKPFSSKIQYKVKVKAQIWLRYLQVOKPTTVFVQILRLIKPMK	180	
Qy	181	DGTYTGTIRSLKLDWNPCTGIWQSIDVKTVLQNLKQPESNLGIEIKAFDETGRDLAVTF	240	
Db	181	DGTYTGTIRSLKLDWNPCTGIWQSIDVKTVLQNLKQPESNLGIEIKAFDETGRDLAVTF	240	
Qy	241	PGPGEDGLNPFLEVRVTDTPKRSRRDRFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIAP	300	
Db	241	PGPGEDGLNPFLEVRVTDTPKRSRRDRFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIAP	300	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.2512 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-8

Perfect score: 2006

Sequence: 1 OKLAVYVYILFMQIAVDPV.....KEQIIVGKIPAMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/iaa/5 COMB.pep.*
- 2: /cgn2_6/prodata/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/iaa/PCUS COMB.pep.*
- 5: /cgn2_6/prodata/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2006	100.0	374	2	US-09-626-896-8
2	2006	100.0	374	2	US-09-841-730-8
3	2006	100.0	375	2	US-09-686-344-23
4	2006	100.0	375	2	US-09-485-046-10
5	2003	99.9	375	2	US-09-252-149B-32
6	1989	99.2	375	2	US-09-686-344-27
7	1989	99.2	375	2	US-09-626-896-18
8	1989	99.2	375	2	US-09-485-046-14
9	1989	99.2	375	2	US-09-841-730-18
10	1978	98.6	375	2	US-09-252-149B-35
11	1976	98.5	375	2	US-09-451-501-23
12	1976	98.5	375	2	US-10-278-803-23
13	1959	97.7	375	2	US-09-451-501-27
14	1959	97.7	375	2	US-10-278-803-27
15	1860	92.7	375	1	US-08-525-596B-14
16	1860	92.7	375	1	US-08-765-875-5
17	1860	92.7	375	2	US-08-795-671-5
18	1860	92.7	375	2	US-09-177-860A-14
19	1860	92.7	375	2	US-09-252-149B-29
20	1860	92.7	375	2	US-09-378-238-14
21	1860	92.7	375	2	US-09-451-501-14
22	1860	92.7	375	2	US-09-629-938-14
23	1860	92.7	375	2	US-09-454-540-5
24	1860	92.7	375	2	US-09-686-344-14
25	1860	92.7	375	2	US-09-626-896-2
26	1860	92.7	375	2	US-09-485-046-4
27	1860	92.7	375	2	US-10-278-803-14

28	1860	92.7	375	2	US-09-841-730-2	Sequence 2, Appli
29	1855	92.5	375	2	US-09-686-344-29	Sequence 29, Appli
30	1855	92.5	375	2	US-09-626-896-14	Sequence 14, Appli
31	1855	92.5	375	2	US-09-841-730-14	Sequence 14, Appli
32	1852	92.3	375	2	US-09-252-149B-32	Sequence 32, Appli
33	1851	92.3	375	2	US-09-451-501-19	Sequence 19, Appli
34	1851	92.3	375	2	US-10-278-803-19	Sequence 19, Appli
35	1850	92.2	375	2	US-09-252-149B-30	Sequence 30, Appli
36	1850	92.2	375	2	US-09-686-344-19	Sequence 19, Appli
37	1850	92.2	375	2	US-09-626-896-10	Sequence 10, Appli
38	1850	92.2	375	2	US-09-485-046-6	Sequence 6, Appli
39	1850	92.2	375	2	US-09-841-730-10	Sequence 10, Appli
40	1842	91.8	376	1	US-08-525-596B-12	Sequence 12, Appli
41	1842	91.8	376	2	US-09-177-860A-12	Sequence 12, Appli
42	1842	91.8	376	2	US-08-891-789B-6	Sequence 6, Appli
43	1842	91.8	376	2	US-09-252-149B-27	Sequence 27, Appli
44	1842	91.8	376	2	US-09-378-238-12	Sequence 12, Appli
45	1842	91.8	376	2	US-09-451-501-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-09-626-896-8
; Sequence 8, Application US/09626896
; Patent No. 6656475
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/626,896
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-626-896-8

Query Match		100.0%;	Score 2006;	DB 2;	Length 374;	
Best Local Similarity		100.0%;	Pred. No. 8.5e-191;			
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QY	1	OKLAVYVYILFMQIAVDPVALDGSQPTENAEKDGKLNACTWRONTKSSRIEAIKIQIL	60			
Db	1	OKLAVYVYILFMQIAVDPVALDGSQPTENAEKDGKLNACTWRONTKSSRIEAIKIQIL	60			
QY	61	SKLRLEQAPNISRDVIKOLLKAPLOQLIDQYDQVORDSSDGSLEDDDYHATTETIITM	120			
Db	61	SKLRLEQAPNISRDVIKOLLKAPLOQLIDQYDQVORDSSDGSLEDDDYHATTETIITM	120			
QY	121	PTESDFLVQMEGKPKCCFFKPFSSKIYKNVKAQLWIYLRQVQKPTTVFVQLIRLIKPKMK	180			
Db	121	PTESDFLVQMEGKPKCCFFKPFSSKIYKNVKAQLWIYLRQVQKPTTVFVQLIRLIKPKMK	180			
QY	181	DGTRYTGIRSLKDMNPCTGIMQSIDVKTIVLQNLKQPESNLGIEIKAFDETRDLAVTF	240			
Db	181	DGTRYTGIRSLKDMNPCTGIMQSIDVKTIVLQNLKQPESNLGIEIKAFDETRDLAVTF	240			
QY	241	PGPGEDGLNPPELVYRVTDTPKSRSDGLDCDEHSTESRCCRYPLTVDFFAFGWDWIAP	300			
Db	241	PGPGEDGLNPPELVYRVTDTPKSRSDGLDCDEHSTESRCCRYPLTVDFFAFGWDWIAP	300			

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.40373 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-6
Perfect score: 2019
Sequence: 1 MTQKQMYVYVFLVLIAG.....KEQIYKIPAMVDRGCS 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: /cgn2_6/prodata/1/pubaa/US10_NEW_PUB pep.*
2: /cgn2_6/prodata/1/pubaa/US06_NEW_PUB pep.*
3: /cgn2_6/prodata/1/pubaa/US07_NEW_PUB pep.*
4: /cgn2_6/prodata/1/pubaa/US08_NEW_PUB pep.*
5: /cgn2_6/prodata/1/pubaa/US09_NEW_PUB pep.*
6: /cgn2_6/prodata/1/pubaa/PCT_NEW_PUB pep.*
7: /cgn2_6/prodata/1/pubaa/US11_NEW_PUB pep.*
8: /cgn2_6/prodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	311.5	15.4	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	242	12.0	366	7	US-11-091-334-9
4	236	11.7	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	10.9	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.8	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication NO. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336 (PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.4%	Score 311.5;	DB 1;	Length 391;
Best Local Similarity	27.4%	Pred. No. 1.2e-24;		
Matches 105;	Conservative 54;	Mismatches 129;	Indels 95;	Gaps 15;
QY	53	RIEAKIQILSKLRLEAFNISKDAIRQLPRAPPLRELIQYDVQVDRSSDGSLED--	110	
DB	45	RIEARGQILSKLRASPPSQGE-----VPPGLPEAVLALYNSTRDVAGESASPEPE	98	
QY	111	---DYHATTET-IITWPTESDFLMQADGPKCCFFKFSKIQNKVVKQAQLWLYL----	161	
DB	99	PEADYYAKEVTRVLJMVETHNEI-----YDFKQSTHMYMFNTS	138	
QY	162	---RAVKTPTTVFQVQLRLIKPMK-----DGTTRYTGIRSLKLDMSPTGTI	203	
DB	139	EUREAVPEPVLUSRAELRLRLKLUKEQHVELYQKYSNNRWYLSNRLAPSDSPE---	195	
QY	204	WOSIDVKTVLQNLKQPNENLGEIKA-----LDENGH-----DLAVTFPGP	245	
DB	196	WLSFDVTGVVRQWLSRGGIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDLATI----	251	
QY	246	GSDGLN-PFLVKVTVTPK-----RSRRDFGLDCDEHSTESRCRCRYPLTVDP-BAFGW	296	
DB	252	--HGMNRPPELLLMATPLERAQHLQSSRRRALDNTNYCFSSSTKNCVCRQLYIDFRKDLGW	309	
QY	297	DWIIAPKRYKANYCSGECEVFVLOQYPHTH---LVHQANPRGSAGPCCTPTKMSPINMLY	353	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.5771 Seconds
(without-alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-6
Perfect score: 2019
Sequence: 1 MIQKPMYIYLVFLIAG.....KEQIIYKIPAMVDRCCS 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*
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5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	376	3	US-09-859-211-25 Sequence 25, Appl
2	2019	100.0	376	3	US-09-841-730-6 Sequence 6, Appl
3	2019	100.0	376	3	US-09-872-856-25 Sequence 25, Appl
4	2019	100.0	376	4	US-10-074-152-28 Sequence 28, Appl
5	2019	100.0	376	4	US-10-278-803-25 Sequence 25, Appl
6	2019	100.0	376	4	US-10-463-973-25 Sequence 25, Appl
7	2019	100.0	376	4	US-10-456-852-12 Sequence 12, Appl
8	1986	98.4	376	3	US-09-859-894A-11 Sequence 11, Appl
9	1986	98.4	376	3	US-09-859-211-12 Sequence 12, Appl
10	1986	98.4	376	3	US-09-841-730-4 Sequence 4, Appl
11	1986	98.4	376	3	US-09-872-856-12 Sequence 12, Appl
12	1986	98.4	376	3	US-09-871-604-10 Sequence 10, Appl
13	1986	98.4	376	4	US-10-074-152-27 Sequence 27, Appl
14	1986	98.4	376	4	US-10-278-803-12 Sequence 12, Appl
15	1986	98.4	376	4	US-10-335-483-12 Sequence 12, Appl
16	1986	98.4	376	4	US-10-251-115-6 Sequence 6, Appl
17	1986	98.4	376	4	US-10-463-973-12 Sequence 12, Appl
18	1986	98.4	376	4	US-10-456-852-2 Sequence 2, Appl
19	1986	98.4	376	4	US-10-459-127-10 Sequence 10, Appl
20	1986	98.4	376	5	US-10-997-809-12 Sequence 12, Appl
21	1986	98.4	376	5	US-10-991-343-12 Sequence 12, Appl
22	1932	95.7	375	4	US-10-278-803-19 Sequence 19, Appl
23	1931	95.6	375	3	US-10-074-152-32 Sequence 32, Appl
24	1928	95.5	375	3	US-09-859-211-29 Sequence 29, Appl
25	1928	95.5	375	3	US-09-841-730-14 Sequence 14, Appl
26	1928	95.5	375	3	US-09-872-856-29 Sequence 29, Appl
27	1928	95.5	375	4	US-10-463-973-29 Sequence 29, Appl

28	1925	95.3	375	3	US-09-454-540-5 Sequence 5, Appl
29	1925	95.3	375	3	US-09-859-211-14 Sequence 14, Appl
30	1925	95.3	375	3	US-09-841-730-2 Sequence 2, Appl
31	1925	95.3	375	3	US-09-872-856-14 Sequence 14, Appl
32	1925	95.3	375	3	US-09-871-604-5 Sequence 5, Appl
33	1925	95.3	375	4	US-10-074-152-29 Sequence 29, Appl
34	1925	95.3	375	4	US-10-278-803-14 Sequence 14, Appl
35	1925	95.3	375	4	US-10-071-499A-1 Sequence 1, Appl
36	1925	95.3	375	4	US-10-335-483-14 Sequence 14, Appl
37	1925	95.3	375	4	US-10-251-115-8 Sequence 8, Appl
38	1925	95.3	375	4	US-10-253-532-130 Sequence 130, Appl
39	1925	95.3	375	4	US-10-366-345-51 Sequence 51, Appl
40	1925	95.3	375	4	US-10-463-973-14 Sequence 14, Appl
41	1925	95.3	375	4	US-10-456-852-4 Sequence 4, Appl
42	1925	95.3	375	4	US-10-459-137-5 Sequence 5, Appl
43	1925	95.3	375	4	US-10-662-438-2 Sequence 2, Appl
44	1925	95.3	375	5	US-10-689-677C-2 Sequence 2, Appl
45	1925	95.3	375	5	US-10-665-374-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-859-211-25
; Sequence 25, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07365/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-859-211-25

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Best Local Similarity		100.0%;	Pred. No. 5.1e-186;		
Matches 376;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	1	MIQKPMYIYLVFLIAGPVDLNE	SREANVEKEGLCNACAWQNT	YSRIBAIKIQ	60
QY	61	ILSKRLTAPNISKDAIRQLP	RAPPLRELIDQYDVRDSDS	GLEDDDYHATTETII	120
DB	61	ILSKRLTAPNISKDAIRQLP	RAPPLRELIDQYDVRDSDS	GLEDDDYHATTETII	120
QY	121	TMPTESDFLWQADGPKCCFF	KSSKIQNKVKAQLWIYLR	AVKTPPTTVFVQILRIKP	180
DB	121	TMPTESDFLWQADGPKCCFF	KSSKIQNKVKAQLWIYLR	AVKTPPTTVFVQILRIKP	180
QY	181	MKDGRYTGIRSLKLDMS	PGTGIWQSIDVKTVLQNL	KQPESNIGIEIKALDENG	HLAV 240

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3488 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-4

Perfect score: 2022

Sequence: 1 MMQKLMYYIYLFMLIAAG.....KEQIYGIKIPAMVDRCGS 376

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2022	100.0	376	2	US-09-177-860A-12 Sequence 12, Appl
3	2022	100.0	376	2	US-08-991-789B-6 Sequence 6, Appl
4	2022	100.0	376	2	US-09-252-149B-27 Sequence 27, Appl
5	2022	100.0	376	2	US-09-378-238-12 Sequence 12, Appl
6	2022	100.0	376	2	US-09-451-501-12 Sequence 12, Appl
7	2022	100.0	376	2	US-09-629-938-12 Sequence 12, Appl
8	2022	100.0	376	2	US-09-686-344-12 Sequence 12, Appl
9	2022	100.0	376	2	US-09-626-896-4 Sequence 4, Appl
10	2022	100.0	376	2	US-09-485-046-2 Sequence 2, Appl
11	2022	100.0	376	2	US-10-278-803-12 Sequence 12, Appl
12	2022	100.0	376	2	US-09-841-730-4 Sequence 4, Appl
13	1986	98.2	376	2	US-09-252-149B-28 Sequence 28, Appl
14	1986	98.2	376	2	US-09-451-501-25 Sequence 25, Appl
15	1986	98.2	376	2	US-09-686-344-25 Sequence 25, Appl
16	1986	98.2	376	2	US-09-626-896-6 Sequence 6, Appl
17	1986	98.2	376	2	US-09-485-046-12 Sequence 12, Appl
18	1986	98.2	376	2	US-10-278-803-25 Sequence 25, Appl
19	1986	98.2	376	2	US-09-841-730-6 Sequence 6, Appl
20	1960	96.9	375	2	US-09-451-501-19 Sequence 19, Appl
21	1960	96.9	375	2	US-10-278-803-19 Sequence 19, Appl
22	1959	96.9	375	2	US-09-252-149B-32 Sequence 32, Appl
23	1956	96.7	375	2	US-09-686-344-29 Sequence 29, Appl
24	1956	96.7	375	2	US-09-626-896-14 Sequence 14, Appl
25	1956	96.7	375	2	US-09-841-730-14 Sequence 14, Appl
26	1953	96.6	375	1	US-08-525-596B-14 Sequence 14, Appl
27	1953	96.6	375	1	US-08-765-875-5 Sequence 5, Appl

28	1953	96.6	375	2	US-08-795-671-5 Sequence 5, Appl
29	1953	96.6	375	2	US-09-177-860A-14 Sequence 14, Appl
30	1953	96.6	375	2	US-09-252-149B-29 Sequence 29, Appl
31	1953	96.6	375	2	US-09-378-238-14 Sequence 14, Appl
32	1953	96.6	375	2	US-09-451-501-14 Sequence 14, Appl
33	1953	96.6	375	2	US-09-629-938-14 Sequence 14, Appl
34	1953	96.6	375	2	US-09-454-540-5 Sequence 5, Appl
35	1953	96.6	375	2	US-09-686-344-14 Sequence 14, Appl
36	1953	96.6	375	2	US-09-626-896-2 Sequence 2, Appl
37	1953	96.6	375	2	US-09-485-046-4 Sequence 4, Appl
38	1953	96.6	375	2	US-10-278-803-14 Sequence 14, Appl
39	1953	96.6	375	2	US-09-841-730-2 Sequence 2, Appl
40	1951	96.5	375	2	US-09-252-149B-30 Sequence 30, Appl
41	1951	96.5	375	2	US-09-686-344-19 Sequence 19, Appl
42	1951	96.5	375	2	US-09-626-896-10 Sequence 10, Appl
43	1951	96.5	375	2	US-09-485-046-6 Sequence 6, Appl
44	1951	96.5	375	2	US-09-841-730-10 Sequence 10, Appl
45	1953	93.6	375	2	US-09-252-149B-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-525-596B-12
; Sequence 12, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-525-596B-12

Query Match 100.0%; Score 2022; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 7.9e-197;
Matches 376; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MMQKLMYYIYLFMLIAAGPVDLNGSRENVKEGLNCAMWQNTYRIEAIKIQ 60
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.5771 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-4
Perfect score: 2022
Sequence: 1 MMQKLMQVYIYLFMLIAAG.....KEQIIYGIKIPAMVDRCGCS 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pgp:
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pgp:
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pgp:
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pgp:
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pgp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2022	100.0	376	3 US-09-859-894A-11	Sequence 11, Appl
2	2022	100.0	376	3 US-09-859-211-12	Sequence 12, Appl
3	2022	100.0	376	3 US-09-841-730-4	Sequence 4, Appl
4	2022	100.0	376	3 US-09-872-856-12	Sequence 12, Appl
5	2022	100.0	376	3 US-09-871-604-10	Sequence 10, Appl
6	2022	100.0	376	4 US-10-074-152-27	Sequence 27, Appl
7	2022	100.0	376	4 US-10-278-803-12	Sequence 12, Appl
8	2022	100.0	376	4 US-10-335-483-12	Sequence 12, Appl
9	2022	100.0	376	4 US-10-251-115-6	Sequence 6, Appl
10	2022	100.0	376	4 US-10-463-973-12	Sequence 12, Appl
11	2022	100.0	376	4 US-10-456-852-2	Sequence 2, Appl
12	2022	100.0	376	4 US-10-459-127-10	Sequence 10, Appl
13	2022	100.0	376	5 US-10-997-809-12	Sequence 12, Appl
14	2022	100.0	376	5 US-10-991-343-12	Sequence 12, Appl
15	1986	98.2	376	3 US-09-859-211-25	Sequence 25, Appl
16	1986	98.2	376	3 US-09-841-730-6	Sequence 6, Appl
17	1986	98.2	376	3 US-09-872-856-25	Sequence 25, Appl
18	1986	98.2	376	4 US-10-074-152-28	Sequence 28, Appl
19	1986	98.2	376	4 US-10-278-803-25	Sequence 25, Appl
20	1986	98.2	376	4 US-10-463-973-25	Sequence 25, Appl
21	1986	98.2	376	4 US-10-456-852-12	Sequence 12, Appl
22	1960	96.9	375	4 US-10-278-803-19	Sequence 19, Appl
23	1959	96.9	375	3 US-10-074-152-32	Sequence 32, Appl
24	1956	96.7	375	3 US-09-859-211-29	Sequence 29, Appl
25	1956	96.7	375	3 US-09-841-730-14	Sequence 14, Appl
26	1956	96.7	375	3 US-09-872-856-29	Sequence 29, Appl
27	1956	96.7	375	4 US-10-463-973-29	Sequence 29, Appl

28	1953	96.6	375	3 US-09-454-540-5	Sequence 5, Appl
29	1953	96.6	375	3 US-09-859-211-14	Sequence 14, Appl
30	1953	96.6	375	3 US-09-841-730-2	Sequence 2, Appl
31	1953	96.6	375	3 US-09-872-856-14	Sequence 14, Appl
32	1953	96.6	375	3 US-09-871-604-5	Sequence 5, Appl
33	1953	96.6	375	4 US-10-074-152-29	Sequence 29, Appl
34	1953	96.6	375	4 US-10-278-803-14	Sequence 14, Appl
35	1953	96.6	375	4 US-10-071-499A-1	Sequence 1, Appl
36	1953	96.6	375	4 US-10-335-483-14	Sequence 14, Appl
37	1953	96.6	375	4 US-10-251-115-8	Sequence 130, Appl
38	1953	96.6	375	4 US-10-253-532-130	Sequence 51, Appl
39	1953	96.6	375	4 US-10-366-345-51	Sequence 14, Appl
40	1953	96.6	375	4 US-10-463-973-14	Sequence 4, Appl
41	1953	96.6	375	4 US-10-456-852-4	Sequence 5, Appl
42	1953	96.6	375	4 US-10-459-127-5	Sequence 2, Appl
43	1953	96.6	375	4 US-10-662-438-2	Sequence 2, Appl
44	1953	96.6	375	5 US-10-689-677C-2	Sequence 2, Appl
45	1953	96.6	375	5 US-10-665-374-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-859-894A-11
; Sequence 11, Application US/09859894A
; Patent No. US20020150577A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; FILE REFERENCE: JHUI200-9
; CURRENT APPLICATION NUMBER: US/09/859,894A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/019,901
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: 08/795,671
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: 08/706,958
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/272,763
; PRIOR FILING DATE: 1994-07-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-859-894A-11

Query Match	100.0%	Score 2022;	DB 3;	Length 376;	
Best Local Similarity	100.0%	Pred. No. 2.4e-188;			
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		Indels	0;	Gaps	0;
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Db	1	MMQKLMQVYIYLFMLIAAGPVDLNEGSRRENVKEGLCNACAWRQNTYRSIEAIKIQ	60		
Qy	61	ILSKLLETAPNISKDAIRQLPRAPRLIDQYDQVDRDSDSGSLEDDDYHATTETII	120		
Db	61	ILSKLLETAPNISKDAIRQLPRAPRLIDQYDQVDRDSDSGSLEDDDYHATTETII	120		
Qy	121	TMPTSDFLMQADGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKTTPTTVFVQILRLIKP	180		
Db	121	TMPTSDFLMQADGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKTTPTTVFVQILRLIKP	180		
Qy	181	MKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNLKQPESNLGIBIKALDENGHLAV	240		
Db	181	MKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNLKQPESNLGIBIKALDENGHLAV	240		
Qy	241	TFPGPESDGLNPFLFVKVVTPTPKRRRDFGLDCDEHSTESRCRCRYPLTVDPFAGWDWII	300		
Db	241	TFPGPESDGLNPFLFVKVVTPTPKRRRDFGLDCDEHSTESRCRCRYPLTVDPFAGWDWII	300		

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.40373 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-4

Perfect score: 2022

Sequence: 1 MMQKLMYVYVLFMLIAAG.....KEQIIYKIPAMVVDRCGS 376

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	306.5	15.2	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	249	12.3	366	7	US-11-091-334-9
4	236	11.7	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.8	139	1	US-10-816-768-88
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.5	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.2	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.0	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

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Best Local Similarity	28.1%	Pred. No. 3.1e-24;		
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QY	53	REAIAKIQILSKRLTAPNISKAIRQLPRAPPLRELIDQVDVORDSSDGSLEDD--	110	
DB	45	RIEARGQILSKRLASPPSQGE-----VPPGPEALVLYNSTRDRVAGESAPEPE	98	
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QY	161	LRPVKTPTTFVQILRLIKPMKDGTRYTGIRSKLDMSPTGIWQSIDVKTVLQNLKQP	220	
DB	158	LRRLKLVQHQVELYQ--KYNNWYLSNRLAPSDSPB---WLSFDVTGVVVRQWLSRG	212	
QY	221	ESNLGIEIKA-----LDENGH-----DLAVTFPGGEGDLN-PFLEVKVYDT	261	
DB	213	GETEGFRLSAHSCSDSRDNTLQVDINGFTTGRGDLATI-----HGMNRPFLLMATPL	266	
QY	262	PK-----RSRDFGLDCDEHSTESRCRYPLTVDF-EAFGWDWIIAPKRYKANCYSGE	313	
DB	267	ERAQHLQSSRRRALDNTNYCFSTERNCCVQRLYIDFRKDLGKWKIHEPKGYHANFCLGP	326	
QY	314	CEVFVFLQKYPHTH---LVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYKIPAMVV	370	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-2

Perfect score: 2018

Sequence: 1 MOKLQCVYILFMLIVAGP.....KEQIIYKIPAMVDRCGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
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- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
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Pred. No. is the number of results predicted by chance to have a
... score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	308.5	15.3	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	238.5	11.8	366	7	US-11-091-334-9
4	232	11.5	364	1	US-10-131-826A-342
5	232	11.5	364	7	US-11-091-334-2
6	231	11.4	429	1	US-10-967-457-74
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-93

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
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43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DANAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.3%	Score 308.5;	DB 1;	Length 391;
Best Local Similarity	26.9%	Pred. No. 1.7e-24;		
Matches 104;	Conservative 55;	Mismatches 132;	Indels 95;	Gaps 15;
QY	49	KSRIBEAIKIQLSKRLTAPNISKDVIRQLPKAPPLRELDQVDVQDRDSDGSLD	108	
Db	42	KRKRIEAIKQILSKRLASPPSQGE-----VPPGFLPEAVLALYNSTRDRVAGESAEP	95	
QY	109	D-----DYHATYET-IITPTESDFLMQVDGKPKCFKSSKIQYKVKQAQMLYL--	160	
Db	96	EPEPEADYYAKETRYLMVETHNEI-----YDKFKQSTHSITMFF	135	
QY	161	-----RPVETPTTVFQILRLIKPMK-----DGTRYTGIRSLKLDNPNP	199	
Db	136	NTSELREANPEFVLLSRAELRLRLKLVQHVVELYQKYSNNRWLSNLLAPSDSPE	195	
QY	200	TGIWQSIDVKTVLQNLWKQFESNLGIEIKA-----LDENGH-----DLAVTF	241	
Db	196	---WLSFDVTGVVQRLSRGEGIEGFLSAHCSDRDNTLQVDINGFTTGRGDLATI-	251	
QY	242	PGEGEGDLN- PFLEVKVTDTPK-----RSRDFGLDCDEHSTESCCRYPLTVDF-BA	292	
Db	252	-----HGMNRPFLMLMATPLERAQHLQSRHRALDNTNYCFSTKNCVCCVRQLYIDPRKD	306	
QY	293	FGWDWIIAPKRYKANYCSGCEPFVLOKYPHPTH---LVHOANPRGSAGPCCTPTQMSPIN	349	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-2

Perfect score: 2018

Sequence: 1 MQKLQICVYILFMLIVAGP.....KEQIYKIPAMVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	375	3	US-09-454-540-5
2	2018	100.0	375	3	US-09-859-211-14
3	2018	100.0	375	3	US-09-841-730-2
4	2018	100.0	375	3	US-09-872-856-14
5	2018	100.0	375	3	US-09-871-604-5
6	2018	100.0	375	4	US-10-074-152-29
7	2018	100.0	375	4	US-10-278-803-14
8	2018	100.0	375	4	US-10-071-499A-1
9	2018	100.0	375	4	US-10-335-483-14
10	2018	100.0	375	4	US-10-251-115-8
11	2018	100.0	375	4	US-10-253-532-130
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19	2018	100.0	375	5	US-10-997-809-14
20	2018	100.0	375	5	US-10-991-343-14
21	2018	100.0	375	6	US-11-019-001-1
22	2018	100.0	376	3	US-09-813-398-38
23	2018	100.0	376	5	US-10-826-324-38
24	2013	99.8	375	3	US-09-859-894A-5
25	2009	99.6	375	4	US-10-278-803-19
26	2008	99.5	375	3	US-09-859-211-19
27	2008	99.5	375	3	US-09-841-730-10

28	2008	99.5	375	3	US-09-872-856-19	Sequence 19, Appl
29	2008	99.5	375	4	US-10-074-152-30	Sequence 30, Appl
30	2008	99.5	375	4	US-10-463-973-19	Sequence 19, Appl
31	2008	99.5	375	4	US-10-456-852-6	Sequence 6, Appl
32	1979	98.1	375	3	US-09-859-211-29	Sequence 29, Appl
33	1979	98.1	375	3	US-09-841-730-14	Sequence 14, Appl
34	1979	98.1	375	3	US-09-872-856-29	Sequence 29, Appl
35	1979	98.1	375	4	US-10-463-973-29	Sequence 29, Appl
36	1976	97.9	375	4	US-10-074-152-32	Sequence 11, Appl
37	1953	96.8	376	3	US-09-859-894A-11	Sequence 12, Appl
38	1953	96.8	376	3	US-09-859-211-12	Sequence 4, Appl
39	1953	96.8	376	3	US-09-841-730-4	Sequence 12, Appl
40	1953	96.8	376	3	US-09-872-856-12	Sequence 12, Appl
41	1953	96.8	376	3	US-09-871-604-10	Sequence 10, Appl
42	1953	96.8	376	4	US-10-074-152-27	Sequence 27, Appl
43	1953	96.8	376	4	US-10-278-803-12	Sequence 12, Appl
44	1953	96.8	376	4	US-10-335-483-12	Sequence 12, Appl
45	1953	96.8	376	4	US-10-251-115-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-454-540-5
; Sequence 5, Application US/09454540
; Patent No. US20010053358A1
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,540
FILING DATE: 06-DEC-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HALL, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-09-454-540-5
Query Match 100.0%; Score 2018; DB 3; Length 375;

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-2
Perfect score: 2018
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2018	100.0	375	2 US-09-177-860A-14	Sequence 14, Appl
5	2018	100.0	375	2 US-09-252-149B-29	Sequence 29, Appl
6	2018	100.0	375	2 US-09-378-238-14	Sequence 14, Appl
7	2018	100.0	375	2 US-09-451-501-14	Sequence 14, Appl
8	2018	100.0	375	2 US-09-629-938-14	Sequence 14, Appl
9	2018	100.0	375	2 US-09-454-540-5	Sequence 5, Appl
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13	2018	100.0	375	2 US-10-278-803-14	Sequence 14, Appl
14	2018	100.0	375	2 US-09-841-730-2	Sequence 2, Appl
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16	2009	99.6	375	2 US-10-278-803-19	Sequence 19, Appl
17	2008	99.5	375	2 US-09-252-149B-30	Sequence 30, Appl
18	2008	99.5	375	2 US-09-686-344-19	Sequence 19, Appl
19	2008	99.5	375	2 US-09-626-896-10	Sequence 10, Appl
20	2008	99.5	375	2 US-09-485-046-6	Sequence 6, Appl
21	2008	99.5	375	2 US-09-841-730-10	Sequence 10, Appl
22	1979	98.1	375	2 US-09-686-344-29	Sequence 29, Appl
23	1979	98.1	375	2 US-09-626-896-14	Sequence 14, Appl
24	1979	98.1	375	2 US-09-841-730-14	Sequence 14, Appl
25	1976	97.9	375	2 US-09-252-149B-32	Sequence 32, Appl
26	1953	96.8	376	1 US-08-525-596B-12	Sequence 12, Appl
27	1953	96.8	376	2 US-09-177-860A-12	Sequence 12, Appl

28	1953	96.8	376	2 US-08-891-789B-6	Sequence 6, Appl
29	1953	96.8	376	2 US-09-252-149B-27	Sequence 27, Appl
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31	1953	96.8	376	2 US-09-451-501-12	Sequence 12, Appl
32	1953	96.8	376	2 US-09-629-938-12	Sequence 12, Appl
33	1953	96.8	376	2 US-09-686-344-12	Sequence 12, Appl
34	1953	96.8	376	2 US-09-626-896-4	Sequence 4, Appl
35	1953	96.8	376	2 US-09-485-046-2	Sequence 2, Appl
36	1953	96.8	376	2 US-10-278-803-12	Sequence 12, Appl
37	1953	96.8	376	2 US-09-841-730-4	Sequence 4, Appl
38	1925	95.4	376	2 US-09-252-149B-28	Sequence 28, Appl
39	1925	95.4	376	2 US-09-451-501-25	Sequence 25, Appl
40	1925	95.4	376	2 US-09-686-344-25	Sequence 25, Appl
41	1925	95.4	376	2 US-09-626-896-6	Sequence 6, Appl
42	1925	95.4	376	2 US-09-485-046-12	Sequence 12, Appl
43	1925	95.4	376	2 US-10-278-803-25	Sequence 25, Appl
44	1925	95.4	376	2 US-09-841-730-6	Sequence 6, Appl
45	1917	95.0	375	2 US-09-686-344-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
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; Sequence 14, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-525-596B-14

Query Match 100.0%; Score 2018; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQLQLCVIYLFMLIVAGPVDLNENSEQENVEKGLCHACTWRQTKSRLEAIKQI 60
|||||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-10

Perfect score: 2016

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2016	100.0	375	2	US-09-252-149B-30
2	2016	100.0	375	2	US-09-686-344-19
3	2016	100.0	375	2	US-09-626-896-10
4	2016	100.0	375	2	US-09-485-046-6
5	2016	100.0	375	2	US-09-841-730-10
6	2008	99.6	375	1	US-08-525-596B-14
7	2008	99.6	375	1	US-08-765-875-5
8	2008	99.6	375	2	US-08-795-671-5
9	2008	99.6	375	2	US-09-177-860A-14
10	2008	99.6	375	2	US-09-252-149B-29
11	2008	99.6	375	2	US-09-378-238-14
12	2008	99.6	375	2	US-09-451-501-14
13	2008	99.6	375	2	US-09-629-938-14
14	2008	99.6	375	2	US-09-454-540-5
15	2008	99.6	375	2	US-09-686-344-14
16	2008	99.6	375	2	US-09-626-896-2
17	2008	99.6	375	2	US-09-485-046-4
18	2008	99.6	375	2	US-10-278-803-14
19	2008	99.6	375	2	US-09-841-730-2
20	2007	99.6	375	2	US-09-451-501-19
21	2007	99.6	375	2	US-10-278-803-19
22	1977	98.1	375	2	US-09-686-344-29
23	1977	98.1	375	2	US-09-626-896-14
24	1977	98.1	375	2	US-09-841-730-14
25	1974	97.9	375	2	US-09-252-149B-32
26	1951	96.8	376	1	US-08-525-596B-12
27	1951	96.8	376	2	US-09-177-860A-12

28	1951	96.8	376	2	US-08-891-789B-6	Sequence 6, Appli
29	1951	96.8	376	2	US-09-252-149B-27	Sequence 27, Appl
30	1951	96.8	376	2	US-09-378-238-12	Sequence 12, Appl
31	1951	96.8	376	2	US-09-451-501-12	Sequence 12, Appl
32	1951	96.8	376	2	US-09-629-938-12	Sequence 12, Appl
33	1951	96.8	376	2	US-09-686-344-12	Sequence 12, Appl
34	1951	96.8	376	2	US-09-626-896-4	Sequence 4, Appli
35	1951	96.8	376	2	US-09-485-046-2	Sequence 2, Appli
36	1951	96.8	376	2	US-10-278-803-12	Sequence 12, Appl
37	1951	96.8	376	2	US-09-841-730-4	Sequence 4, Appli
38	1923	95.4	376	2	US-09-252-149B-28	Sequence 28, Appl
39	1923	95.4	376	2	US-09-451-501-25	Sequence 25, Appl
40	1923	95.4	376	2	US-09-686-344-25	Sequence 25, Appl
41	1923	95.4	376	2	US-09-626-896-6	Sequence 6, Appli
42	1923	95.4	376	2	US-09-485-046-12	Sequence 12, Appl
43	1923	95.4	376	2	US-10-278-803-25	Sequence 25, Appl
44	1923	95.4	376	2	US-09-841-730-6	Sequence 6, Appli
45	1915	95.0	375	2	US-09-686-344-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-252-149B-30
; Sequence 30, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: VERTEBRATE SUBJECTS
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-252-149B-30

Query Match Similarity 100.0%; Score 2016; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.4e-195;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQKQLCVYIYLFMLIVAGPVDLNENGEKVENKEGKLCNACTWRONTKSSRIEAIKIQI 60

Db 1 MQKQLCVYIYLFMLIVAGPVDLNENGEKVENKEGKLCNACTWRONTKSSRIEAIKIQI 60

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Db 61 LSKRLTETAPNISKDAIRQLLPKAPPRELIDQYDVRDDSDGSLDDDDYHATTETIIT 120

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Db 121 MPTESDFLMQVGGKPKCFKFSKIQYNKVKAQLMIYLRPVETPTTVFVQILRLIKPM 180

Qy 181 KDGTRYTGIRSLKLDMPGPGIWSIDVKTVLQNLKOPESNLGIEIKALDENGHDLAIV 240

Db 181 KDGTRYTGIRSLKLDMPGPGIWSIDVKTVLQNLKOPESNLGIEIKALDENGHDLAIV 240

Qy 241 FPGGEDGLNPFLEVKVYTDTPKRRRDFGLDCDSEHSTESRCRYPYLTVDPEALGWDWIIA 300

Db 241 FPGGEDGLNPFLEVKVYTDTPKRRRDFGLDCDSEHSTESRCRYPYLTVDPEALGWDWIIA 300

Qy 301 PKRYKANCSECEBFVFLQKYPHTLHVQANPRGAGCCPTTKXGSPINMLYFNGKEQII 360

Db 301 PKRYKANCSECEBFVFLQKYPHTLHVQANPRGAGCCPTTKXGSPINMLYFNGKEQII 360

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3488 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-6

Perfect score: 2019

Sequence: 1 MIQKPMQVYIYLFVLIAG.....KEQIIYKIPAMVVDRCGS 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	376	2	US-09-252-149B-28
2	2019	100.0	376	2	US-09-451-501-25
3	2019	100.0	376	2	US-09-626-344-25
4	2019	100.0	376	2	US-09-626-896-6
5	2019	100.0	376	2	US-09-485-046-12
6	2019	100.0	376	2	US-10-278-803-25
7	2019	100.0	376	2	US-09-841-730-6
8	1986	98.4	376	1	US-08-525-596B-12
9	1986	98.4	376	2	US-09-177-860A-12
10	1986	98.4	376	2	US-08-891-789B-6
11	1986	98.4	376	2	US-09-252-149B-27
12	1986	98.4	376	2	US-09-378-238-12
13	1986	98.4	376	2	US-09-451-501-12
14	1986	98.4	376	2	US-09-629-938-12
15	1986	98.4	376	2	US-09-626-896-4
16	1986	98.4	376	2	US-09-485-046-2
17	1986	98.4	376	2	US-10-278-803-12
18	1986	98.4	376	2	US-09-841-730-4
19	1986	98.4	376	2	US-09-451-501-19
20	1932	95.7	375	2	US-10-278-803-19
21	1932	95.7	375	2	US-09-252-149B-32
22	1931	95.6	375	2	US-09-626-344-29
23	1928	95.5	375	2	US-09-626-896-14
24	1928	95.5	375	2	US-09-841-730-14
25	1928	95.5	375	1	US-08-525-596B-14
26	1925	95.3	375	1	US-08-765-875-5
27	1925	95.3	375	1	US-08-765-875-5

28	1925	95.3	375	2	US-08-795-671-5	Sequence 5, Appl
29	1925	95.3	375	2	US-09-177-860A-14	Sequence 14, Appl
30	1925	95.3	375	2	US-09-252-149B-29	Sequence 29, Appl
31	1925	95.3	375	2	US-09-378-238-14	Sequence 14, Appl
32	1925	95.3	375	2	US-09-451-501-14	Sequence 14, Appl
33	1925	95.3	375	2	US-09-629-938-14	Sequence 14, Appl
34	1925	95.3	375	2	US-09-454-540-5	Sequence 5, Appl
35	1925	95.3	375	2	US-09-686-344-14	Sequence 14, Appl
36	1925	95.3	375	2	US-09-626-896-2	Sequence 2, Appl
37	1925	95.3	375	2	US-09-485-046-4	Sequence 4, Appl
38	1925	95.3	375	2	US-10-278-803-14	Sequence 14, Appl
39	1925	95.3	375	2	US-09-841-730-2	Sequence 2, Appl
40	1923	95.2	375	2	US-09-252-149B-30	Sequence 30, Appl
41	1923	95.2	375	2	US-09-686-344-19	Sequence 19, Appl
42	1923	95.2	375	2	US-09-626-896-10	Sequence 10, Appl
43	1923	95.2	375	2	US-09-485-046-6	Sequence 6, Appl
44	1923	95.2	375	2	US-09-841-730-10	Sequence 10, Appl
45	1865	92.4	375	2	US-09-252-149B-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-252-149B-28
; Sequence 28, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-252-149B-28

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Gaps	0;						
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Db	61	ILSKRLTAPNISKDAIRQLPRAP	RLIQQYVQRDDSDGSLDDDYHATTETII	120			
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Qy	181	MDQTRTYGIRSLKLDMSPGT	GIWQSIDVKTVLQWLKQPSNLGIEIKALDEN	GHDLAV	240		
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